GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: September 9, 2002, 19:06:22 ; Search time 129.72 Seconds
(without alignments)
6731.630 Million cell updates/sec

Title: US-09-762-311-4_COPY_176_3730
Perfect score: 3555
Sequence: 1 atggaaccaataacattcac.....tcccacactgtccaggcctt 3555

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2510.4	70.6	4039	1	US-08-363-300-1	Sequence 1, Appli
c	2	57.8	1.6	7218	1	US-08-232-463-14	Sequence 14, Appl
	3	45.4	1.3	9515	1	US-08-920-812-13	Sequence 13, Appl
	4	45.4	1.3	9515	1	US-08-920-827-13	Sequence 13, Appl
	5	45.4	1.3	9515	1	US-08-921-177-13	Sequence 13, Appl
	6	45.4	1.3	9515	1	US-08-362-577C-13	Sequence 13, Appl
	7	45.4	1.3	9515	2	US-08-920-828-13	Sequence 13, Appl
	8	45	1.3	8201	1	US-08-253-155A-9	Sequence 9, Appli
	9	41	1.2	1957	1	US-08-295-060-3	Sequence 3, Appli
	10	40.8	1.1	1030	3	US-08-858-003-2	Sequence 2, Appli
	11	40.8	1.1	1030	3	US-09-078-166-2	Sequence 2, Appli
	12	40.8	1.1	1030	4	US-08-997-467-2	Sequence 2, Appli
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	14	40.6	1.1	2279	3	US-08-814-052-17	Sequence 17, Appl
	15	40.6	1.1	2300	3	US-08-814-052-18	Sequence 18, Appl
	16	40.6	1.1	3183	2	US-08-939-218A-1	Sequence 1, Appli
	17	40.6	1.1	3192	1	US-08-940-661A-1	Sequence 1, Appli
	18	40.6	1.1	3192	2	US-09-083-485-1	Sequence 1, Appli
c	19	40.6	1.1	3358	3	US-09-248-571-2	Sequence 2, Appli
	20	40.4	1.1	4134	4	US-09-162-021B-1	Sequence 1, Appli
	21	40	1.1	1962	2	US-08-919-421A-1	Sequence 1, Appli
	22	40	1.1	1962	4	US-09-342-819-1	Sequence 1, Appli
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	24	39.2	1.1	3192	1	US-08-706-037-26	Sequence 26, Appl
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c	45	38.8	1.1	1069	4	US-09-372-422A-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-08-363-300-1
; Sequence 1, Application US/08363300
; Patent No. 5700927
; GENERAL INFORMATION:
; APPLICANT: Zon, Leonard and Richardson, Paul
; TITLE OF INVENTION: Tbc1 Gene and Uses Thereof
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,300
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04590/009001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4039 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 403..3829
US-08-363-300-1

Query Match 70.6%; Score 2510.4; DB 1; Length 4039;
Best Local Similarity 83.7%; Pred. No. 0;
Matches 2949; Conservative 0; Mismatches 536; Indels 37; Gaps 8;

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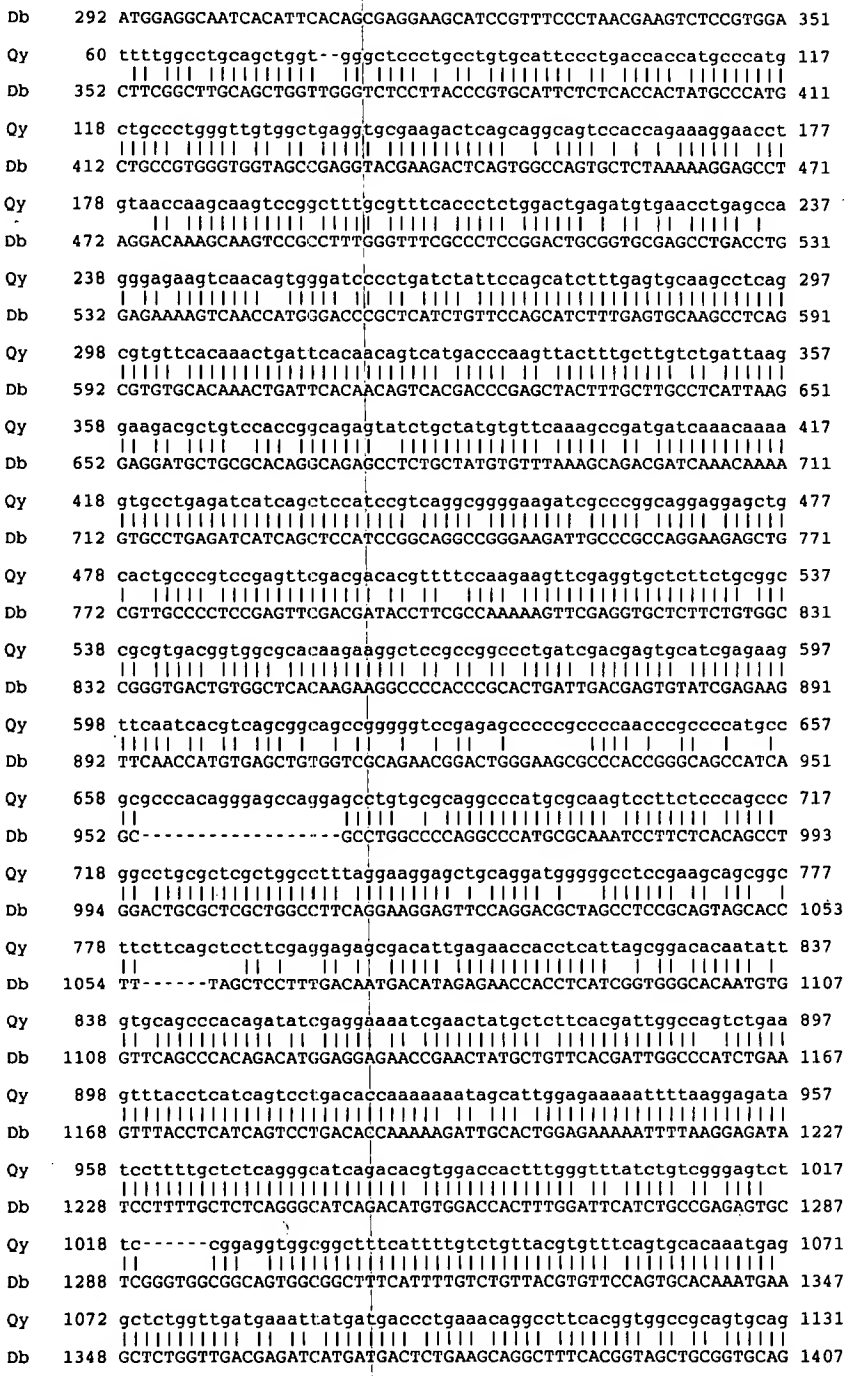
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RESULT   2
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-Fls
US-08-232-463-14


  Query Match             1.6%;  Score 57.8;  DB 1;  Length 7218;
  Best Local Similarity   2.9%;  Pred. No. 9.7e-06;
  Matches   11;  Conservative  225;  Mismatches  147;  Indels    0;  Gaps    0;

Qy   1198 gagaggatagagggaatgaattcttccaaaacaaaactagaactgcaaaagcacctgacg 1257
          ::::::: :::::::: :::       :::: ::::  ::::  : ::::: :   :: :
Db   1428 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1369
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Qy   1258 acattaaccaatcaggagcaggcgactatttttgaagaggttcagaaattgagaccgaga 1317
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Db   1368 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1309

Qy   1318 aatgagcagcgagagaatgaattgattatttcttttctgagatgtttatatgaagagaaa 1377
          :: ::: :: ::::::: ::: | ::  :          :::: :   : : :::::::::
Db   1308 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1249

Qy   1378 cagaaagaacacatccatattggggagatgaagcagacatcgcagatggcagcagagaat 1437
           :::::::: : :   : :  :::::: :::: ::: :  : ::: :: :: ::::::
Db   1248 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1189

Qy   1438 attggaagtgaattaccacccagtgccactcgatttaggctagatatgctgaaaaacaaa 1497
          :  ::::: :::  :  :  :: :  :   ::  :::  ::: : :  :::::: :::
Db   1188 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1129

Qy   1498 gcaaagagatctttaacagagtctttagaaagtattttgtcccggggtaataaagccaga 1557
          : :::::::     :: ::::    :::::: :    :    :::: :: ::::  :::
Db   1128 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1069

Qy   1558 ggcctgcaggaacactccatcag 1580
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Db   1068 RRATCGCAAGCTCCCTCGACCTG 1046


RESULT   3
US-08-920-812-13
; Sequence 13, Application US/08920812
; Patent No. 5763188
;  GENERAL INFORMATION:
;    APPLICANT:  Ohno, Tsuneya
;    APPLICANT:  Matsuhisa, Akio
;    APPLICANT:  Uehara, Hirotsugu
;    APPLICANT:  Eda, Soji
;    TITLE OF INVENTION:  Probe for Diagnosing Infectious Disease
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/920,812
;      FILING DATE:  29-AUG-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/362,577
;      FILING DATE:  27-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rin-Laures, Li-Hsien
;      REGISTRATION NUMBER:  33,547
;      REFERENCE/DOCKET NUMBER:  19036/32420
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9515 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Pseudomonas aeruginosa
;      STRAIN:  Clinical Isolate P2-2
US-08-920-812-13


  Query Match             1.3%;  Score 45.4;  DB 1;  Length 9515;
  Best Local Similarity   46.2%;  Pred. No. 0.033;
  Matches  151;  Conservative    0;  Mismatches  176;  Indels    0;  Gaps    0;

Qy    438 catccgtcaggcggggaagatcgcccggcaggaggagctgcactgcccgtccgagttcga 497
          |||  |  || ||| || |  |||| || |    ||  | | | || |  || |  ||
Db    802 CATGGGCAAGCCGGTGATGGACGCCTGGAACATCGATGTACCCGGCGCCGCCCACGTCTT 861

Qy    498 cgacacgttttccaagaagttcgaggtgctcttctgcggccgcgtgacggtggcgcacaa 557
          || |  || | |  | |   ||||   ||||| |  |     || | |||  || ||  |
Db    862 CGCCTGGTATGCGGAAAGCCTCGACAAGCTCTACGACCAGGTCGCGCCGGCCGCCCAGCA 921

Qy    558 gaaggctccgccggccctgatcgacgagtgcatcgagaagttcaatcacgtcagcggcag 617
          ||       | |          ||    |      | ||    |      ||     | | |
Db    922 GACCCTGGCCACCATTACCCGCGTGCCGCTGGGGGTGATCGGCGCGGTGGTGCCGTGGAA 981

Qy    618 ccgggggtccgagagcccccgccccaacccgccccatgccgcgcccacagggagccagga 677
          |     |  ||| |   ||  |   || |   |||  |||  | || | || | |  ||
Db    982 CTTCCCGCTCGACATGGCCGCCTGGAAGCTCGCCCCGGCCCTGGCCGCCGGCAACTCGGT 1041

Qy    678 gcctgtgcgcaggcccatgcgcaagtccttctcccagcccggcctgcgctcgctggcctt 737
          |     |      | ||  ||    | | ||||||    |   |||||  |  |||||| |
Db   1042 GGTGCTCAAGCCGGCCGAGCAGTCGCCGTTCTCCGCCCTGCGCCTGGCCGAGCTGGCCCT 1101

Qy    738 taggaaggagctgcaggatgggggcct 764
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Db   1102 GGAGGCGGGGGTGCCGGAAGGCGTGCT 1128


RESULT   4
US-08-920-827-13
; Sequence 13, Application US/08920827
; Patent No. 5770375
;  GENERAL INFORMATION:
;    APPLICANT:  Ohno, Tsuneya
;    APPLICANT:  Matsuhisa, Akio
;    APPLICANT:  Uehara, Hirotsugu
;    APPLICANT:  Eda, Soji
;    TITLE OF INVENTION:  Probe for Diagnosing Infectious Disease
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/920,827
;      FILING DATE:  29-AUG-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/362,577
;      FILING DATE:  27-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rin-Laures, Li-Hsien
;      REGISTRATION NUMBER:  33,547
;      REFERENCE/DOCKET NUMBER:  19036/32420
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  9515 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Pseudomonas aeruginosa
;      STRAIN:  Clinical Isolate P2-2
US-08-920-827-13


  Query Match             1.3%;  Score 45.4;  DB 1;  Length 9515;
  Best Local Similarity   46.2%;  Pred. No. 0.033;
  Matches  151;  Conservative    0;  Mismatches  176;  Indels    0;  Gaps    0;

Qy    438 catccgtcaggcggggaagatcgcccggcaggaggagctgcactgcccgtccgagttcga 497
          |||  |  || ||| || |  |||| || |    ||  | | | || |  || |  ||
Db    802 CATGGGCAAGCCGGTGATGGACGCCTGGAACATCGATGTACCCGGCGCCGCCCACGTCTT 861

Qy    498 cgacacgttttccaagaagttcgaggtgctcttctgcggccgcgtgacggtggcgcacaa 557
          || |  || | |  | |   ||||   ||||| |  |     || | |||  || ||  |
Db    862 CGCCTGGTATGCGGAAAGCCTCGACAAGCTCTACGACCAGGTCGCGCCGGCCGCCCAGCA 921

Qy    558 gaaggctccgccggccctgatcgacgagtgcatcgagaagttcaatcacgtcagcggcag 617
          ||      |  |          ||     |       | ||     |       ||      | |
Db    922 GACCCTGGCCACCATTACCCGCGTGCCGCTGGGGGTGATCGGCGCGGTGGTGCCGTGGAA 981

Qy    618 ccgggggtccgagagcccccgcccccaacccgccccatgccgcgcccacagggagccagga 677
          |     |  ||| |   ||  |   || |   |||  |||  | || | || | |  ||
Db    982 CTTCCCGCTCGACATGGCCGCCTGGAAGCTCGCCCCGGCCCTGGCCGCCGGCAACTCGGT 1041

Qy    678 gcctgtgcgcaggcccatgcgcaagtccttctcccagcccggcctgcgctcgctggcctt 737
          |  |      | ||  ||  |  | | ||||||   |   |||||  |  |||||||  |
Db   1042 GGTGCTCAAGCCGGCCGAGCAGTCGCCGTTCTCCGCCCTGCGCCTGGCCGAGCTGGCCCT 1101

Qy    738 taggaaggagctgcaggatgggggcct 764
            |  || | ||| ||| || ||  ||
Db   1102 GGAGGCGGGGGTGCCGGAAGGCGTGCT 1128


RESULT   5
US-08-921-177-13
; Sequence 13, Application US/08921177
; Patent No. 5798211
;  GENERAL INFORMATION:
;    APPLICANT:  Ohno, Tsuneya
;    APPLICANT:  Matsuhisa, Akio
;    APPLICANT:  Uehara, Hirotsugu
;    APPLICANT:  Eda, Soji
;    TITLE OF INVENTION:  Probe for Diagnosing Infectious Disease
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/921,177
;      FILING DATE:  29-AUG-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/362,577
;      FILING DATE:  27-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rin-Laures, Li-Hsien
;      REGISTRATION NUMBER:  33,547
;      REFERENCE/DOCKET NUMBER:  19036/32420
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9515 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Pseudomonas aeruginosa
;      STRAIN:  Clinical Isolate P2-2
US-08-921-177-13


  Query Match             1.3%;  Score 45.4;  DB 1;  Length 9515;
  Best Local Similarity   46.2%;  Pred. No. 0.033;
  Matches  151;  Conservative    0;  Mismatches  176;  Indels    0;  Gaps    0;

Qy    438 catccgtcaggcggggaagatcgcccggcaggaggagctgcactgcccgtccgagttcga 497
          |||  |  || ||| || |  |||| || |    ||  | | | || |  || |  ||
Db    802 CATGGGCAAGCCGGTGATGGACGCCTGGAACATCGATGTACCCGGCGCCGCCCACGTCTT 861

Qy    498 cgacacgttttccaagaagttcgaggtgctcttctgcggccgcgtgacggtggcgcacaa 557
          || |  || | |  | |   ||||   ||||| |  |     || | |||  || ||  |
Db    862 CGCCTGGTATGCGGAAAGCCTCGACAAGCTCTACGACCAGGTCGCGCCGGCCGCCCAGCA 921

Qy    558 gaaggctccgccggccctgatcgacgagtgcatcgagaagttcaatcacgtcagcggcag 617
          ||      |  |          ||     |       | ||     |       ||      | |
Db    922 GACCCTGGCCACCATTACCCGCGTGCCGCTGGGGGTGATCGGCGCGGTGGTGCCGTGGAA 981

Qy    618 ccgggggtccgagagcccccgcccccaacccgccccatgccgcgcccacagggagccagga 677
          |     |  ||| |   ||  |   || |   |||  |||  | || | || | |  ||
Db    982 CTTCCCGCTCGACATGGCCGCCTGGAAGCTCGCCCCGGCCCTGGCCGCCGGCAACTCGGT 1041

Qy    678 gcctgtgcgcaggcccatgcgcaagtccttctcccagcccggcctgcgctcgctggcctt 737
          |  |      | ||  ||  |  | | ||||||   |   |||||  |  |||||||  |
Db   1042 GGTGCTCAAGCCGGCCGAGCAGTCGCCGTTCTCCGCCCTGCGCCTGGCCGAGCTGGCCCT 1101

Qy    738 taggaaggagctgcaggatgggggcct 764
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Db   1102 GGAGGCGGGGGTGCCGGAAGGCGTGCT 1128


RESULT   6
US-08-362-577C-13
; Sequence 13, Application US/08362577C
; Patent No. 5807673
;  GENERAL INFORMATION:
;    APPLICANT:  Ohno, Tsuneya
;    APPLICANT:  Matsuhisa, Akio
;    APPLICANT:  Uehara, Hirotsugu
;    APPLICANT:  Eda, Soji
;    TITLE OF INVENTION:  Probe for Diagnosing Infectious Disease
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/362,577C
;      FILING DATE:  27-MAR-1995
```

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;     CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rin-Laures, Li-Hsien
;      REGISTRATION NUMBER:  33,547
;      REFERENCE/DOCKET NUMBER:  19036/32420
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9515 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Pseudomonas aeruginosa
;      STRAIN:  Clinical Isolate P2-2
US-08-362-577C-13


  Query Match             1.3%;  Score 45.4;  DB 1;  Length 9515;
  Best Local Similarity   46.2%;  Pred. No. 0.033;
  Matches  151;  Conservative    0;  Mismatches  176;  Indels    0;  Gaps    0;

Qy    438 catccgtcaggcggggaagatcgcccggcaggaggagctgcactgcccgtccgagttcga 497
          |||  |  || ||| || |  |||| || |    ||  | | | || |  || |  ||
Db    802 CATGGGCAAGCCGGTGATGGACGCCTGGAACATCGATGTACCCGGCGCCGCCCACGTCTT 861

Qy    498 cgacacgttttccaagaagttcgaggtgctcttctgcggccgcgtgacggtggcgcacaa 557
          || |  || | |  | |   ||||  ||||| |  |     || | |||  || ||  |
Db    862 CGCCTGGTATGCGGAAAGCCTCGACAAGCTCTACGACCAGGTCGCGCCGGCCGCCCAGCA 921

Qy    558 gaaggctccgccggccctgatcgacgagtgcatcgagaagttcaatcacgtcagcggcag 617
          ||      |  |          ||    |       | ||     |       ||      | |
Db    922 GACCCTGGCCACCATTACCCGCGTGCCGCTGGGGGTGATCGGCGCGGTGGTGCCGTGGAA 981

Qy    618 ccgggggtccgagagccccccgccccaacccgccccatgccgcgcccacagggagccagga 677
          |   |  ||| |   ||  |  || |   ||| ||| | || | || | |  ||
Db    982 CTTCCCGCTCGACATGGCCGCCTGGAAGCTCGCCCCGGCCCTGGCCGCCGGCAACTCGGT 1041

Qy    678 gcctgtgcgcaggcccatgcgcaagtccttctcccagcccggcctgcgctcgctggcctt 737
          |    |      | ||  ||   | | ||||||   |   |||||  |  ||||||| |
Db   1042 GGTGCTCAAGCCGGCCGAGCAGTCGCCGTTCTCCGCCCTGCGCCTGGCCGAGCTGGCCCT 1101

Qy    738 taggaaggagctgcaggatgggggcct 764
            |  || | ||| ||| || |  ||
Db   1102 GGAGGCGGGGGTGCCGGAAGGCGTGCT 1128


RESULT   7
US-08-920-828-13
; Sequence 13, Application US/08920828
; Patent No. 5853998
;  GENERAL INFORMATION:
;    APPLICANT:  Ohno, Tsuneya
;    APPLICANT:  Matsuhisa, Akio
;    APPLICANT:  Uehara, Hirotsugu
;    APPLICANT:  Eda, Soji
;    TITLE OF INVENTION:  Probe for Diagnosing Infectious Disease
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/920,828
;      FILING DATE:  29-AUG-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/362,577
;      FILING DATE:  27-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rin-Laures, Li-Hsien
;      REGISTRATION NUMBER:  33,547
;      REFERENCE/DOCKET NUMBER:  19036/32420
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9515 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Pseudomonas aeruginosa
;      STRAIN:  Clinical Isolate P2-2
US-08-920-828-13


  Query Match             1.3%;  Score 45.4;  DB 2;  Length 9515;
  Best Local Similarity   46.2%;  Pred. No. 0.033;
  Matches  151;  Conservative    0;  Mismatches  176;  Indels    0;  Gaps    0;

Qy    438 catccgtcaggcggggaagatcgcccggcaggaggagctgcactgcccgtccgagttcga 497
          |||  |  || ||| || |  |||| || |    ||  | | | || |  || |  ||
Db    802 CATGGGCAAGCCGGTGATGGACGCCTGGAACATCGATGTACCCGGCGCCGCCCACGTCTT 861

Qy    498 cgacacgttttccaagaagttcgaggtgctcttctgcggccgcgtgacggtggcgcacaa 557
          || |  || | |  | |   ||||  ||||| |  |     || | |||  || ||  |
Db    862 CGCCTGGTATGCGGAAAGCCTCGACAAGCTCTACGACCAGGTCGCGCCGGCCGCCCAGCA 921

Qy    558 gaaggctccgccggccctgatcgacgagtgcatcgagaagttcaatcacgtcagcggcag 617
          ||      |  |          ||    |       | ||     |       ||      | |
Db    922 GACCCTGGCCACCATTACCCGCGTGCCGCTGGGGGTGATCGGCGCGGTGGTGCCGTGGAA 981

Qy    618 ccgggggtccgagagccccccgccccaacccgccccatgccgcgcccacagggagccagga 677
          |   |  ||| |   ||  |  || |   ||| ||| | || | || | |  ||
Db    982 CTTCCCGCTCGACATGGCCGCCTGGAAGCTCGCCCCGGCCCTGGCCGCCGGCAACTCGGT 1041

Qy    678 gcctgtgcgcaggcccatgcgcaagtccttctcccagcccggcctgcgctcgctggcctt 737
          |    |      | ||  ||   | | ||||||   |   |||||  |  ||||||| |
Db   1042 GGTGCTCAAGCCGGCCGAGCAGTCGCCGTTCTCCGCCCTGCGCCTGGCCGAGCTGGCCCT 1101

Qy    738 taggaaggagctgcaggatgggggcct 764
            |  || | ||| ||| || |  ||
Db   1102 GGAGGCGGGGGTGCCGGAAGGCGTGCT 1128


RESULT   8
US-08-253-155A-9
; Sequence 9, Application US/08253155A
; Patent No. 5691147
;  GENERAL INFORMATION:
;    APPLICANT:  Gyuris, Jeno
;    APPLICANT:  Draetta, Giulio
;    TITLE OF INVENTION:  CDK4 Binding Proteins
;    NUMBER OF SEQUENCES:  95
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
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;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII(text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/253,155A
;      FILING DATE:  02-JUN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36,709
;      REFERENCE/DOCKET NUMBER:  MII-028
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8201 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-253-155A-9


  Query Match             1.3%;  Score 45;  DB 1;  Length 8201;
  Best Local Similarity   53.0%;  Pred. No. 0.039;
  Matches   96;  Conservative    0;  Mismatches   85;  Indels    0;  Gaps    0;

Qy    2549 ttgaccttgggcgaaccttttcctacacacccatacttctctgcccagcttggagcaggac 2608
           | ||| |  ||   || ' | |  |  ||    | |||    |  |    ||||||    |
Db    2133 TGGACGTGAGGACGACTCTCCGGAACCATGTCTTCTTTAGGGATCGATATGGAGCCAAGC 2192

Qy    2609 agctatcgctttacaacattttgaaggcctactcacttctagaccaggaagtgggatatt 2668
           ||       || | | ||||   |   |||||| ||        ||| ||| ||||| || |
Db    2193 AGAGGGAACTATTCTACATCCTCCTGGCCTATTCGGAGTATAACCCGGAGGTGGGCTACT 2252

Qy    2669 gccaaggtctcagctttgtagcaggcattttgcttcttcatatgagtgaggaagaggcgt 2728
           ||   |  || |||    |  | | | | || || ||| || ||  |||||| || || |
Db    2253 GCAGGGACCTGAGCCACATCACCGCCTTGTTCCTCCTTTATCTGCCTGAGGAGGACGCAT 2312

Qy    2729 t 2729
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Db    2313 T 2313


RESULT   9
US-08-295-060-3
; Sequence 3, Application US/08295060
; Patent No. 5659123
;  GENERAL INFORMATION:
;    APPLICANT:  VAN RIE, Jeroen
;    APPLICANT:  JANSENS, Stefan
;    APPLICANT:  PERFEROEN, Marnix
;    TITLE OF INVENTION:  NEW DIABROTICA TOXINS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  P.O. Box 1404
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  United States
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/295,060
;      FILING DATE:  26-AUG-1994
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Crane-Feury, Sharon E
;      REGISTRATION NUMBER:  36,113
;      REFERENCE/DOCKET NUMBER:  010830-052
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 836-6620
;      TELEFAX:  (703) 836-2021
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1957 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  13..1947
US-08-295-060-3


  Query Match             1.2%;  Score 41;  DB 1;  Length 1957;
  Best Local Similarity   47.9%;  Pred. No. 0.22;
  Matches  113;  Conservative    0;  Mismatches  123;  Indels    0;  Gaps    0;

Qy     488 ccgagttcgacgacacgttttccaagaagttcgaggtgctcttctgcggccgcgtgacgg 547
           || ||  | ||||||       |||   |  ||  |||  ||    | ||  ||    |
Db    1322 CCCAGACCTACGACAGCNNNCGCAACGTGGGCGCTGTGAGCTGGGACAGCATCGACCAGC 1381

Qy     548 tggcgcacaagaaggctccgccggccctgatcgacgagtgcatcgagaagttcaatcacg 607
           || | | | |||    |       | |||||    | |  | || | |  || | ||  |||
Db    1382 TGCCTCCCGAGACCACCGACGAGCCCCTGGAGAAGGGCTACAGCCACCAGCTGAACTACG 1441

Qy     608 tcagcggcagccgggggtccgagagcccccgccccaacccgccccatgccgcgcccacag 667
           | |   ||  || |  |   |  |||    || ||| |||    |   ||  | ||
Db    1442 TGATGTGCTTCCTGATGCAGGGCAGCAGGGGCACCATCCCAGTGCTGACCTGGACCCACA 1501

Qy     668 ggagccaggagcctgtgcgcaggcccatgcgcaagtccttctcccagcccggcctg 723
            ||||  |||     |   || |  |    |||||    || ||||||    ||||
Db    1502 AGAGCGTGGACTTCTTCAACATGATCGACAGCAAGAAGATCACCCAGCTGCCCCTG 1557


RESULT  10
US-08-858-003-2
; Sequence 2, Application US/08858003
; Patent No. 6060234
;  GENERAL INFORMATION:
;    APPLICANT:  Katz, Leonard
;    APPLICANT:  Stassi, Diane L.
;    APPLICANT:  Summers Jr., Richard G.
;    APPLICANT:  Ruan, Xiaoan
;    APPLICANT:  Pereda-Lopez, Ana
;    APPLICANT:  Kakavas, Stephan J.
;    TITLE OF INVENTION:  NOVEL POLYKETIDE DERIVATIVES
;    TITLE OF INVENTION:  AND RECOMBINANT METHODS FOR MAKING SAME
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories
;      STREET:  100 Abbott Park Rd.
;      CITY:  Abbott Park
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60064-3500
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/858,003
;      FILING DATE:  16-MAY-1979
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;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dianne Casuto
;      REGISTRATION NUMBER:  P-40,943
;      REFERENCE/DOCKET NUMBER:  4952.US.P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (847)-938-3137
;      TELEFAX:  (847)-938-2623
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1030 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-858-003-2


  Query Match             1.1%;  Score 40.8;  DB 3;  Length 1030;
  Best Local Similarity   50.0%;  Pred. No. 0.18;
  Matches  102;  Conservative    0;  Mismatches  102;  Indels    0;  Gaps    0;

Qy    440 tccgtcaggcggggaagatcgcccggcaggaggagctgcactgcccgtccgagttcgacg 499
          ||   |||||||    | |||||  | ||      |||  | | | || ||||  | |||
Db    203 TCACACAGGCGGCTCTGTTCGCCGTGGAGACCTCCCTGTTCCGGCTGTTCGAGGCCCACG 262

Qy    500 acacgttttccaagaagttcgaggtgctcttctgcggccgcgtgacggtggcgcacaaga 559
            |    |  || |  |  ||   |  | || |  ||||   ||||| | ||| |||  |
Db    263 GCCTCGTCCCCGACTACCTCATCGGCCACTCCATCGGCGAAGTGACCGCGGCCCACCTGG 322

Qy    560 aggctccgccggccctgatcgacgagtgcatcgagaagttcaatcacgtcagcggcagcc 619
            |     |  |  |||   |||| |||| ||  |     | | | || | ||   |  |
Db    323 CCGGGGTCCTCGATCTGGCGGACGCGTGCGTCCTGGTCGCCCACCGCGGCCGCCTGATGC 382

Qy    620 gggggtccgagagcccccgcccca 643
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Db    383 AGTCGGCCCGGGCCGGCGGCGCGA 406


RESULT  11
US-09-078-166-2
; Sequence 2, Application US/09078166
; Patent No. 6063561
;  GENERAL INFORMATION:
;    APPLICANT:  Katz, Leonard
;    APPLICANT:  Stassi, Diane L.
;    APPLICANT:  Summers Jr., Richard G.
;    APPLICANT:  Ruan, Xiaoan
;    APPLICANT:  Pereda-Lopez, Ana
;    APPLICANT:  Kakavas, Stephan J.
;    TITLE OF INVENTION:  NOVEL POLYKETIDE DERIVATIVES
;    TITLE OF INVENTION:  AND RECOMBINANT METHODS FOR MAKING SAME
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories
;      STREET:  100 Abbott Park Rd.
;      CITY:  Abbott Park
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60064-3500
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/078,166
;      FILING DATE:  16-MAY-1979
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dianne Casuto
;      REGISTRATION NUMBER:  P-40,943
;      REFERENCE/DOCKET NUMBER:  4952.US.P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (847)-938-3137
;      TELEFAX:  (847)-938-2623
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1030 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-09-078-166-2


  Query Match             1.1%;  Score 40.8;  DB 3;  Length 1030;
  Best Local Similarity   50.0%;  Pred. No. 0.18;
  Matches  102;  Conservative    0;  Mismatches  102;  Indels    0;  Gaps    0;

Qy    440 tccgtcaggcggggaagatcgcccggcaggaggagctgcactgcccgtccgagttcgacg 499
          ||   |||||||    | |||||  | ||      |||  | | | || ||||  | |||
Db    203 TCACACAGGCGGCTCTGTTCGCCGTGGAGACCTCCCTGTTCCGGCTGTTCGAGGCCCACG 262

Qy    500 acacgttttccaagaagttcgaggtgctcttctgcggccgcgtgacggtggcgcacaaga 559
            |    |  || |  |  ||   |  | || |  ||||   ||||| | ||| |||  |
Db    263 GCCTCGTCCCCGACTACCTCATCGGCCACTCCATCGGCGAAGTGACCGCGGCCCACCTGG 322

Qy    560 aggctccgccggccctgatcgacgagtgcatcgagaagttcaatcacgtcagcggcagcc 619
            |     |  |  |||   |||| |||| ||  |     | | | || | ||   |  |
Db    323 CCGGGGTCCTCGATCTGGCGGACGCGTGCGTCCTGGTCGCCCACCGCGGCCGCCTGATGC 382

Qy    620 gggggtccgagagcccccgcccca 643
            | | ||  |  |  | || | ||
Db    383 AGTCGGCCCGGGCCGGCGGCGCGA 406


RESULT  12
US-08-997-467-2
; Sequence 2, Application US/08997467
; Patent No. 6200813
;  GENERAL INFORMATION:
;    APPLICANT:  Katz, Leonard
;    APPLICANT:  Stassi, Diane L.
;    APPLICANT:  Summers Jr., Richard G.
;    APPLICANT:  Ruan, Xiaoan
;    APPLICANT:  Pereda-Lopez, Ana
;    APPLICANT:  Kakavas, Stephan J.
;    TITLE OF INVENTION:  NOVEL POLYKETIDE DERIVATIVES
;    TITLE OF INVENTION:  AND RECOMBINANT METHODS FOR MAKING SAME
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories
;      STREET:  100 Abbott Park Rd.
;      CITY:  Abbott Park
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60064-3500
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/997,467
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/858,003
;      FILING DATE:  16-MAY-1997
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;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dianne Casuto
;      REGISTRATION NUMBER:  P-40,943
;      REFERENCE/DOCKET NUMBER:  4952.US.P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (847)-938-3137
;      TELEFAX:  (847)-938-2623
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1030 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-997-467-2


  Query Match             1.1%;  Score 40.8;  DB 4;  Length 1030;
  Best Local Similarity   50.0%;  Pred. No. 0.18;
  Matches  102;  Conservative    0;  Mismatches  102;  Indels    0;  Gaps    0;

Qy    440 tccgtcaggcggggaagatcgcccggcaggaggagctgcactgcccgtccgagttcgacg 499
          ||   |||||||    | |||||  | ||      |||  | | | || ||||  | |||
Db    203 TCACACAGGCGGCTCTGTTCGCCGTGGAGACCTCCCTGTTCCGGCTGTTCGAGGCCCACG 262

Qy    500 acacgttttccaagaagttcgaggtgctcttctgcggccgcgtgacggtggcgcacaaga 559
          |    | || |  |  ||  |  | || |  ||||   ||||| | ||| |||  |
Db    263 GCCTCGTCCCCGACTACCTCATCGGCCACTCCATCGGCGAAGTGACCGCGGCCCACCTGG 322

Qy    560 aggctccgccggccctgatcgacgagtgcatcgagaagttcaatcacgtcagcggcagcc 619
            |    |  |  |||   |||| |||| ||  |     | | | || | ||   |  |
Db    323 CCGGGGTCCTCGATCTGGCGGACGCGTGCGTCCTGGTCGCCCACCGCGGCCGCCTGATGC 382

Qy    620 gggggtccgagagcccccgcccca 643
            |  | ||  |  |  | || | |
Db    383 AGTCGGCCCGGGCCGGCGGCGCGA 406


RESULT  13
US-08-814-052-19
; Sequence 19, Application US/08814052
; Patent No. 6015783
;  GENERAL INFORMATION:
;    APPLICANT:  von der Osten, Claus
;    APPLICANT:  Cherry, Joel R.
;    APPLICANT:  Bjornvad, Mads E.
;    APPLICANT:  Vind, Jesper
;    APPLICANT:  Rasmussen, Michael Dolberg
;    TITLE OF INVENTION:  PROCESS FOR REMOVAL OR BLEACHING OF SOILING
;    TITLE OF INVENTION:  OR STAINS FROM CELLULOSIC FABRIC
;    NUMBER OF SEQUENCES:  55
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 6015783o No. 6015783disk of No. 6015783th America, Inc.
;      STREET:  405 Lexington Avenue, Suite 6400
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10174-6401
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/814,052
;      FILING DATE:  06-MAR-1997
;      CLASSIFICATION:  510
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lambiris, Elias J
;      REGISTRATION NUMBER:  33,728
;      REFERENCE/DOCKET NUMBER:  4684.204-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-867-0123
;      TELEFAX:  212-878-9655
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2249 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-814-052-19


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  Matches  109;  Conservative    0;  Mismatches  114;  Indels    0;  Gaps    0;

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Qy    534 cggccgcgtgacggtggcgcacaagaaggctccgccggccctgatcgacgagtgcatcga 593
          |||| ||  | |   ||   |    ||||| |||   | ||  | |  |  | | ||
Db   1294 CGGCGGCCCGCCCACGGACGAGGGCAAGGCCCCGGTCGACCACAACTGCCTGGACCTCCC 1353

Qy    594 gaagttcaatcacgtcagcggcagccgggggtccgagagcccccgccccaacccgcccca 653
            ||  |||| | ||||   | | ||   | ||  ||||  |  | |||| | |||| |
Db   1354 CAACCTCAAGCCCGTCGTGGCCCGCGACGTGCCCCTGAGCGGCTTCGCCAAGCGGCCCGA 1413

Qy    654 tgccgcgcccacagggagccaggagcctgtgcgcaggcccatg 696
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Db   1414 CAACACGCTCGACGTCACCCTCGACACCACGGGCACGCCCCTG 1456


RESULT  14
US-08-814-052-17
; Sequence 17, Application US/08814052
; Patent No. 6015783
;  GENERAL INFORMATION:
;    APPLICANT:  von der Osten, Claus
;    APPLICANT:  Cherry, Joel R.
;    APPLICANT:  Bjornvad, Mads E.
;    APPLICANT:  Vind, Jesper
;    APPLICANT:  Rasmussen, Michael Dolberg
;    TITLE OF INVENTION:  PROCESS FOR REMOVAL OR BLEACHING OF SOILING
;    TITLE OF INVENTION:  OR STAINS FROM CELLULOSIC FABRIC
;    NUMBER OF SEQUENCES:  55
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 6015783o No. 6015783disk of No. 6015783th America, Inc.
;      STREET:  405 Lexington Avenue, Suite 6400
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10174-6401
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/814,052
;      FILING DATE:  06-MAR-1997
;      CLASSIFICATION:  510
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lambiris, Elias J
;      REGISTRATION NUMBER:  33,728
;      REFERENCE/DOCKET NUMBER:  4684.204-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-867-0123
;      TELEFAX:  212-878-9655
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2279 base pairs
;      TYPE:  nucleic acid
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;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-814-052-17


  Query Match             1.1%;  Score 40.6;  DB 3;  Length 2279;
  Best Local Similarity   48.9%;  Pred. No. 0.32;
  Matches  109;  Conservative    0;  Mismatches  114;  Indels    0;  Gaps    0;

Qy     474 gctgcactgcccgtccgagttcgacgacacgttttccaagaagttcgaggtgctcttctg 533
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Db    1340 GCTCTGCGGCGGCTCCAGGAATCCCTACCCGGCCGCCATCTTCCACTACGCCGGCGCCCC 1399

Qy     534 cggccgcgtgacggtggcgcacaagaaggctccgccggccctgatcgacgagtgcatcga 593
           ||||  ||  | |   ||   |   |||||  |||   | ||  | |  |  |  |  | ||
Db    1400 CGGCGGCCCGCCCACGGACGAGGGCAAGGCCCCGGTCGACCACAACTGCCTGGACCTCCC 1459

Qy     594 gaagttcaatcacgtcagcggcagccgggggtccgagagcccccgccccaacccgcccca 653
            ||  |||| | ||||   | | ||  | | ||  ||||  |  | |||| | |||| |
Db    1460 CAACCTCAAGCCCGTCGTGGCCCGCGACGTGCCCCTGAGCGGCTTCGCCAAGCGGCCCGA 1519

Qy     654 tgccgcgcccacagggagccaggagcctgtgcgcaggcccatg 696
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Db    1520 CAACACGCTCGACGTCACCCTCGACACCACGGGCACGCCCCTG 1562


RESULT  15
US-08-814-052-18
; Sequence 18, Application US/08814052
; Patent No. 6015783
;  GENERAL INFORMATION:
;    APPLICANT:  von der Osten, Claus
;    APPLICANT:  Cherry, Joel R.
;    APPLICANT:  Bjornvad, Mads E.
;    APPLICANT:  Vind, Jesper
;    APPLICANT:  Rasmussen, Michael Dolberg
;    TITLE OF INVENTION:  PROCESS FOR REMOVAL OR BLEACHING OF SOILING
;    TITLE OF INVENTION:  OR STAINS FROM CELLULOSIC FABRIC
;    NUMBER OF SEQUENCES:  55
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 6015783o No. 6015783disk of No. 6015783th America, Inc.
;      STREET:  405 Lexington Avenue, Suite 6400
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10174-6401
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/814,052
;      FILING DATE:  06-MAR-1997
;      CLASSIFICATION:  510
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lambiris, Elias J
;      REGISTRATION NUMBER:  33,728
;      REFERENCE/DOCKET NUMBER:  4684.204-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-867-0123
;      TELEFAX:  212-878-9655
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2300 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-814-052-18


  Query Match             1.1%;  Score 40.6;  DB 3;  Length 2300;
  Best Local Similarity   48.9%;  Pred. No. 0.32;
  Matches  109;  Conservative    0;  Mismatches  114;  Indels    0;  Gaps    0;

Qy     474 gctgcactgcccgtccgagttcgacgacacgttttccaagaagttcgaggtgctcttctg 533
           |||   | ||   |||  |    | || ||    |||       | | |    |  |
Db    1234 GCTCTGCGGCGGCTCCAGGAATCCCTACCCGGCCGCCATCTTCCACTACGCCGGCGCCCC 1293

Qy     534 cggccgcgtgacggtggcgcacaagaaggctccgccggccctgatcgacgagtgcatcga 593
           ||||  ||  | |   ||   |   |||||  |||   | ||  | |  |  |  |  | ||
Db    1294 CGGCGGCCCGCCCACGGACGAGGGCAAGGCCCCGGTCGACCACAACTGCCTGGACCTCCC 1353

Qy     594 gaagttcaatcacgtcagcggcagccgggggtccgagagcccccgccccaacccgcccca 653
            ||  |||| | ||||   | | ||  | | ||  ||||  |  | |||| | |||| |
Db    1354 CAACCTCAAGCCCGTCGTGGCCCGCGACGTGCCCCTGAGCGGCTTCGCCAAGCGGCCCGA 1413

Qy     654 tgccgcgcccacagggagccaggagcctgtgcgcaggcccatg 696
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Db    1414 CAACACGCTCGACGTCACCCTCGACACCACGGGCACGCCCCTG 1456


Search completed:  September  9, 2002, 19:07:56
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: September 9, 2002, 16:41:06 ; Search time 5191.84 Seconds
(without alignments)
9241.748 Million cell updates/sec

Title: US-09-762-311-4_COPY_176_3730
Perfect score: 3555
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
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6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	833.6	23.4	1001	10	Z78359	Z78359 HSZ78359 Hu
	2	826.6	23.3	1051	10	BM479578	BM479578 AGENCOURT
	3	819.2	23.0	1007	10	BM016445	BM016445 603641252
	4	782.4	22.0	784	10	BG828092	BG828092 602753463
	5	741.8	20.9	835	10	BG759286	BG759286 602710975
	6	738.8	20.8	800	10	BG746377	BG746377 602703644
	7	737.4	20.7	1121	10	BM476629	BM476629 AGENCOURT
	8	729.8	20.5	1109	10	BM460573	BM460573 AGENCOURT
	9	722.2	20.3	952	10	BE299948	BE299948 600944494
	10	713.8	20.1	838	10	BI907513	BI907513 603065640
	11	705	19.8	807	10	BG120498	BG120498 602346815
	12	701	19.7	832	10	BM014940	BM014940 603640877
	13	689.8	19.4	851	9	AL570425	AL570425 AL570425
	14	683.4	19.2	754	10	BE300005	BE300005 600944594
	15	682.6	19.2	892	10	BE561889	BE561889 601346094
	16	678.6	19.1	686	10	BG769758	BG769758 602744658
	17	675	19.0	1108	10	BG326728	BG326728 602425604
	18	671.8	18.9	978	10	BG029927	BG029927 602297271
	19	669.6	18.8	670	9	AL557623	AL557623 AL557623
c	20	669.4	18.8	857	9	AL544177	AL544177 AL544177
	21	668.4	18.8	750	10	BI084159	BI084159 602869636
	22	664.6	18.7	795	10	BE560184	BE560184 601346896
	23	661	18.6	661	9	AL046787	AL046787 DKFZp434M
	24	661	18.6	948	10	BG258116	BG258116 602379212
	25	659.2	18.5	672	10	BE675153	BE675153 7f03d07.x
	26	652.8	18.4	806	9	AW043925	AW043925 wy82b07.x
	27	648.8	18.3	665	9	AW173375	AW173375 xj78g07.x
	28	647.8	18.2	812	10	BI758489	BI758489 603023334
	29	641	18.0	1161	10	BM466841	BM466841 AGENCOURT
	30	637.8	17.9	773	10	BE561312	BE561312 601344450
c	31	636.4	17.9	862	10	BI910369	BI910369 603068025
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	33	632.4	17.8	761	10	BF797592	BF797592 602257390
	34	632	17.8	753	10	BF305442	BF305442 601892937
	35	630	17.7	722	10	BE560392	BE560392 601347108
	36	628	17.7	748	10	BG424359	BG424359 602447963
	37	624.4	17.6	627	9	AW772402	AW772402 hn73a08.x
	38	621.2	17.5	626	9	AW239183	AW239183 xb37a10.y
	39	612	17.2	623	10	BE884440	BE884440 601510724
	40	604.4	17.0	649	10	BE513375	BE513375 601315702
	41	597	16.8	605	9	AW732976	AW732976 bb18b11.y
	42	596.2	16.8	622	10	BE514108	BE514108 601315945
	43	592.4	16.7	774	10	BI763670	BI763670 603049558
	44	590.2	16.6	952	10	BG424757	BG424757 602453405
	45	589.4	16.6	758	10	BG166636	BG166636 602339021

ALIGNMENTS

RESULT 1
Z78359/c
LOCUS Z78359 1001 bp mRNA linear EST 28-JUL-1999
DEFINITION HSZ78359 Human fetal brain S. Meier-Ewert Homo sapiens cDNA clone 3.114 (CEPH) 5', mRNA sequence.
ACCESSION Z78359
VERSION Z78359.1 GI:1495132
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1001)
AUTHORS Neri,C., Albanese,V., Lebre,A.S., Holbert,S., Saada,C., Bougueleret,L., Meier-Ewert,S., LeGall,I., Millasseau,P., Bui,H., Giudicelli,C., Massart,C., Guillou,S., Gervy,P., Poullier,E., Rigault,P., Weissenbach,J., Lennon,G., Chumakov,I., Dausset,J., Lehrach,H., Cohen,D. and Cann,H.M.
TITLE Survey of CAG/CTG repeats in human cDNAs representing new genes: candidates for inherited neurological disorders
JOURNAL Hum. Mol. Genet. 5 (7), 1001-1009 (1996)
MEDLINE 96414310
COMMENT Contact: Neri C.
Fondation Jean Dausset - CEPH
27 Rue Juliette Dodu, 75010 Paris, France
Related sequence: Z78360
5'-sequence (upper strand).
FEATURES Location/Qualifiers
source 1. .1001
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="3.114 (CEPH)"
/clone_lib="Human fetal brain S. Meier-Ewert"
/tissue_type="brain"
/dev_stage="fetus"
/note="cDNA library of S. Meier-Ewert, Max Planck Inst.f.Mol.Genetics, Berlin, FRG"
BASE COUNT 237 a 229 c 231 g 272 t 32 others
ORIGIN

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  Best Local Similarity  93.5%;  Pred. No. 2.2e-197;
  Matches  937;  Conservative    0;  Mismatches   56;  Indels    9;  Gaps    8;

Qy   2146 acatctcgtgagctccgagagctgtggcaaaaggctattcttcaacagatactgctgctt 2205
          ||||||||||||||||||||||||| | ||||||||||||||||||||| ||||||||
Db   1001 ACATCTCGTGAGCTCCGAGAGCTGTGCCTAAAGGCTATTCTTCAACAGATNCTGCTGCTN 942

Qy   2206 agaatggagaaggaaaatcagaagctccaagcctctgaaaatgatttgctgaacaagcgc 2265
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Db    941 AGAATGGAGAAGGAAAATCAGAAGCTCCAAGCCTCTGAAAATGATTTGCTGAACAAGCGC 882

Qy   2266 ctgaagctcgattatgaagaaattactccctgtcttaaagaagtaactacagtgtgggaa 2325
          ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    881 CTGAAGCTCGATTATGAAGAAATNACTCCCTGTCTTAAAGAAGTAACTACAGTGTGGGAA 822

Qy   2326 aagatgcttagcactccaggaagat--caaaaattaagtttgacatggaaaaaatgcact 2383
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Db    821 AAGATGCTTAGCACTCCAGGAAGATCCCANAAATTAAGTTTGACATGGAAAAAATGCACT 762

Qy   2384 cggctgttgggc-aaggtgtgccacgtcatcaccgaggtgaaatctggaaa-tttctagc 2441
          || |||||||||| ||||||||||||||||||||||||||||||||||| ||||||||
Db    761 CGACTGTTGGGCTAAGGTGTGCCACGTCATCACCGAGGTGAAATCTGGAAATTTTCTAGC 702

Qy   2442 tgagcaa-ttccaccttaaacaccagtttcccagcaaacagcagccaaaggatgtgccat 2500
          ||||||| ||||||| |||||||||||||||||||||||||||||||||||||||||||
Db    701 TGAGCAATTTCCACCGTAAACACCAGTTTCCCAGCANACAGCAGCCANAGGATGTGCCAT 642

Qy   2501 acaaagaactcttaaagcagctgacttcccagcagcatgcgattcttattgaccttgggc 2560
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||| |
Db    641 ACAAAGAACTCTTNAAGCAGCTGACTTCCCAGCAGCATGCGATTCTTATTGACCTTGGNC 582

Qy   2561 gaacctttcctacacacccatacttctctgcccagcttggagcaggacagctatcgcttt 2620
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Db    581 GAACCTTTCCTACACACCCATACTTCTCTGCCCAGCTTGGAGCAGGACAGCTATCGCTTT 522

Qy   2621 acaacattttgaaggcctactcacttctagaccaggaagtgggatattgccaaggtctca 2680
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Db    521 ACAACATTTTGAAGGCCTACTCACTTCTAGACCAGGAAGTGGGATATTGCCAAGGTCTCA 462

Qy   2681 gctttgtagcaggcattttgcttcttcatatgagtgaggaagaggcgtttaaaatgctca 2740
          |||||||| |||||||||||| |||||||||||||||||||||||||| ||| |||||||
Db    461 GCTTTGTACCAGGCATTTTGCGTCTTCATATGAGTGAGGAAGAGGCGTGTAAGATGCTCA 402

Qy   2741 agtttctgatgtttgacatggggctgcggaaacagtatcggccagacatgattattttac 2800
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Db    401 AGTTTCTGATG-TTGACATGGGCCTNNGGGNACAGNATCGGCCAGACATGATTATTTTAC 343

Qy   2801 agatccagatgtaccagctctcgaggttgcttcatgattaccacagagacctctacaatc 2860
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Db    342 AGANCCAGATGTACCANCTCTCGGGGTTNCNTNATGATTACCACAGAGACCTCAACAATC 283

Qy   2861 acctggaggagcacgagatcggccccagcctctacgctg-ccccctggttcctcaccatg 2919
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Db    282 ACCTGGAGGAGGNCGAGATCGGCCCCAGCCTCTACGCTGCCCCCCCTGGTTCCTCACCATG 223

Qy   2920 tttgcctcacagttcccgctgggattcgtagccagagtctttgatatgatttttcttcag 2979
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Db    222 TTTGCCTCACAGTTGCCGCTGGGATTCGTATNCAGAGNCTTTGANATGATTTTTCTTCAG 163

Qy   2980 ggaacagaggtcatatttaaagtggctttaagtctgttgggaagccataagcccttgatt 3039
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Db    162 GGAACAGAGGTCATATTTAAAGTGGCGGNAAGNCTGNTGGGAANCCATAAGCCNGTGATT 103

Qy   3040 ctgcagcatgaaaacctagaaa-ccatagttgactttataaaaagcacgctacccaacct 3098
          |||||  |||||||||||||||  ||| ||| ||||||| |||||||||||||||||||
Db    102 CTGCANCATGAAAACCTAGAANGCCAGAGTNGACTTTATGTAAAGCACGCTACCCAACCT 43

Qy   3099 tggcttggtacagatggaa-aagaccatcaatcaggtatttg 3139
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Db     42 TGGCGTGGTNNAGATGGAAGNAGACCATCAATCAGGTAGGTG 1
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RESULT   2
BM479578
LOCUS       BM479578                1051 bp    mRNA    linear   EST 05-FEB-2002
DEFINITION  AGENCOURT_6464998 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5577183
            5', mRNA sequence.
ACCESSION   BM479578
VERSION     BM479578.1  GI:18528620
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1051)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12330  row: d  column: 16
            High quality sequence stop: 662.
FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_92"
                     /tissue_type="embryonal carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 2.5 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
BASE COUNT      296 a    278 c    234 g    243 t
ORIGIN
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  Query Match            23.3%;  Score 826.6;  DB 10;  Length 1051;
  Best Local Similarity  95.8%;  Pred. No. 1.3e-195;
  Matches  892;  Conservative    0;  Mismatches   34;  Indels    5;  Gaps    4;

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Qy   2511 cttaaagcagctgacttcccagcagcatgcgattcttattgaccttgggcgaacctttcc 2570
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CTTAAAGCAGCTGACTTCCCAGCAGCATGCGATTCTTATTGACCTTGGGCGAACCTTTCC 120

Qy   2571 tacacacccatacttctctgcccagcttggagcaggacagctatcgctttacaacatttt 2630
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TACACACCCATACTTCTCTGCCCAGCTTGGAGCAGGACAGCTATCGCTTTACAACATTTT 180

Qy   2631 gaaggcctactcacttctagaccaggaagtgggatattgccaaggtctcagctttgtagc 2690
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Db    181 GAAGGCCTACTCACTTCTAGACCAGGAAGTGGGATATTGCCAAGGTCTCAGCTTTGTAGC 240

Qy   2691 aggcattttgcttcttcatatgagtgaggaagaggcgtttaaaatgctcaagtttctgat 2750
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Db    241 AGGCATTTTGCTTCTTCATATGAGTGAGGAAGAGGCGTTTAAAATGCTCAAGTTTCTGAT 300

Qy   2751 gtttgacatggggctgcggaaacagtatcggccagacatgattattttacagatccagat 2810
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Db    301 GTTTGACATGGGGCTGCGGAAACAGTATCGGCCAGACATGATTATTTTACAGATCCAGAT 360
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Qy   2811 gtaccagctctcgaggttgcttcatgattaccacagagacctctacaatcacctggagga 2870
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Db    361 GTACCAGCTCTCGAGGTTGCTTCATGATTACCACAGAGACCTCTACAATCACCTGGAGGA 420

Qy   2871 gcacgagatcggccccagcctctacgctgccccctggttcctcaccatgtttgcctcaca 2930
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Db    421 GCACGAGATCGGCCCCAGCCTCTACGCTGCCCCCTGGTTCCTCACCATGTTTGCCTCACA 480

Qy   2931 gttcccgctgggattcgtagccagagtctttgatatgatttttcttcagggaacagaggt 2990
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Db    481 GTTCCCGCTGGGATTCGTAGCCAGAGTCTTTGATATGATTTTTCTTCAGGGAACAGAGGT 540

Qy   2991 catatttaaagtggctttaagtctgttgggaagccataagcccttgattctgcagcatga 3050
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Db    541 CATATTTAAAGTGGCTTTAAGTCTGTTGGGAAGCCATAAGCCCTTGATTCTGCAGCATGA 600

Qy   3051 aaacctagaaaccatagttgactttataaaaagcacgctacccaaccttggcttggtaca 3110
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Db    601 AAACCTAGAAACCATAGTTGACTTTATAAAAAGCACGCTACCCAACCTTGGCTTGGTACA 660

Qy   3111 gatggaaaagaccatcaatcaggtatttgaaatggacatcgctaaacagttacaagctta 3170
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Db    661 GATGGAAAAGACCATCAATCAGGTATTTGAAATGGACATCGCTAAACAGTTACAAGCTTA 720

Qy   3171 tgaagttgagtaccacgtccttcaagaagaacttatcgattcctctcctctcagtgacaa 3230
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Db    721 TGAAGTTGAGTACCACGTCCTTCAAGAAGAACTTATCGATTCCTCTCCTCTCAGTGACAA 780

Qy   3231 ccaaagaatggataaattagagaaaaccaacagcagcttacgcaaacagaaccttgacct 3290
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Db    781 CC-AAGAATGGATAATTAGAGAAAACCAACAGCAGGCTTACGCAAACGAAACCTTGACCC 839

Qy   3291 ccttgaacagttgcaggt-ggcaaatggtaggatccaaagccttg--aggccaccattga 3347
           | |  |||||||||||| ||| |||||||| |||||||||| ||   | || |||| ||
Db    840 TCCTTGACAGTTGCAGGTGGGCCAATGGTAAGATCCAAAGCCCTGGAGGCCCCCCATGGA 899

Qy   3348 gaagct-cctgagcagtgagagcaagctgaa 3377
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RESULT   3
BM016445
LOCUS       BM016445                1007 bp    mRNA    linear   EST 30-OCT-2001
DEFINITION  603641252F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5417148 5',
            mRNA sequence.
ACCESSION   BM016445
VERSION     BM016445.1  GI:16530799
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1007)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12064  row: h  column: 13
            High quality sequence stop: 822.
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                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 1.383 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
BASE COUNT      274 a    246 c    255 g    231 t      1 others
ORIGIN


  Query Match             23.0%;  Score 819.2;  DB 10;  Length 1007;
  Best Local Similarity   95.1%;  Pred. No. 8.9e-194;
  Matches  910;  Conservative    0;  Mismatches   39;  Indels    8;  Gaps    6;

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Qy   2592 ccagcttggagcaggacagctatcgctttacaacattttgaaggcctactcacttctaga 2651
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Qy   2652 ccaggaagtgggatattgccaaggtctcagctttgtagcaggcattttgcttcttcatat 2711
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Db    121 CCAGGAAGTGGGATATTGCCAAGGTCTCAGCTTTGTAGCAGGCANTTTGCTTCTTCATAT 180

Qy   2712 gagtgaggaagaggcgtttaaaatgctcaagtttctgatgtttgacatggggctgcggaa 2771
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Qy   2772 acagtatcggccagacatgattattttacagatccagatgtaccagctctcgaggttgct 2831
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Db    241 ACAGTATCGGCCAGACATGATTATTTTACAGATCCAGATGTACCAGCTCTCGAGGTTGCT 300

Qy   2832 tcatgattaccacagagacctctacaatcacctggaggagcacgagatcggccccagcct 2891
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Db    301 TCATGATTACCACAGAGACCTCTACAATCACCTGGAGGAGCACGAGATCGGCCCCAGCCT 360

Qy   2892 ctacgctgccccctggttcctcaccatgtttgcctcacagttcccgctgggattcgtagc 2951
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Db    361 CTACGCTGCCCCCTGGTTCCTCACCATGTTTGCCTCACAGTTCCCGCTGGGATTCGTAGC 420

Qy   2952 cagagtctttgatatgatttttcttcagggaacagaggtcatatttaaagtggctttaag 3011
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Db    421 CAGAGTCTTTGATATGATTTTTCTTCAGGGAACAGAGGTCATATTTAAAGTGGCTTTAAG 480

Qy   3012 tctgttgggaagccataagcccttgattctgcagcatgaaaacctagaaaccatagttga 3071
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Qy   3072 ctttataaaaagcacgctacccaaccttggcttggtacagatggaaaagaccatcaatca 3131
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Db    541 CTTTATAAAAAGCACGCTACCCAACCTTGGCTTGGTACAGATGGAAAAGACCATCAATCA 600

Qy   3132 ggtatttgaaatggacatcgctaaacagttacaagcttatgaagttgagtaccacgtcct 3191
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GGTATCTGAAATGGACATCGCTAAACAGTTACAAGCTTATGAAGTTGAGTACCACGTCCT 660

Qy   3192 tcaagaagaacttatcgattcctctcctctcagtgacaaccaaagaatggataa-attag 3250
          |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db    661 TCAAGAAGAACTTATCGATTCCTCTCCTCTCAGTGACAACCAAAGAATGGATAACCTTAG 720

Qy   3251 agaaaaccaacagcagcttacgcaaacagaaccttgacctccttgaacagttgca-ggtg 3309
          |||||||||||||||| ||||||||||||||||  ||||||||||||||||| |||| |||
Db    721 AGAAAACCAACAGCAG-TTACGCAAACAGAACCTTGGACTCCTTGAACAGTTGCAGGGTG 779

Qy   3310 gcaaatggtaggatccaaagccttgaggccaccattgagaa--gctcctgagcagtgaga 3367
          |||||||||||||||||||||||||||||| |||||||||     || ||||||||||||
Db    780 GCAAATGGTAGGATCCAAAGCCTTGAGGCCCCCATTGAGAAAGCTCCCGGAGCAGTGAGA 839

Qy   3368 gcaag--ctgaagcaggccatgcttacc-ttagaactggagcggtcggccctgctgcaga 3424
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          |||||    |||||||||||||||||| ||||||||||    |   | ||||||||||||
Db    840 GCAAGGCTGGAAGCAGGCCATGCTTACCTTTAGAACTGGGAGCGGTCGGCCTGCTGCAGA 899

Qy   3425 cggtggaggagctgcggcggcggagcgcagagcccagcgaccgggagcctgagtgca 3481
          |||||||||| ||||||  | ||| |    |  ||      |||||||| |||||||
Db    900 CGGTGGAGGAACTGCGGGCGGGGAACCGCAAAGCCCAGCGACGGGAGCCGGAGTGCA 956


RESULT   4
BG828092
LOCUS       BG828092                 784 bp    mRNA    linear   EST 22-MAY-2001
DEFINITION  602753463F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4906191 5',
            mRNA sequence.
ACCESSION   BG828092
VERSION     BG828092.1  GI:14175679
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 784)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1808  row: n  column: 16
            High quality sequence stop: 784.
FEATURES             Location/Qualifiers
     source          1. .784
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:4906191"
                     /clone_lib="NIH_MGC_17"
                     /tissue_type="rhabdomyosarcoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
                     Site_2: XhoI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G).  Size-selected >500bp
                     for average insert size 1.8kb.  Library constructed by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      236 a    190 c    182 g    176 t
ORIGIN


  Query Match           22.0%;  Score 782.4;  DB 10;  Length 784;
  Best Local Similarity  99.9%;  Pred. No. 1.3e-184;
  Matches  783;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   1859 ggaaacttatgaggtatcactcagtgagcacagagacgcctcatgaacgaaaggactttg 1918
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GGAAACTTATGAGGTATCACTCAGTGAGCACAGAGACGCCTCATGAACGAAAGGACTTTG 60

Qy   1919 aatccaaagcaaaccatcttggtgattctggtgggactcctgtgaagacccggaggcatt 1978
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AATCCAAAGCAAACCATCTTGGTGATTCTGGTGGGACTCCTGTGAAGACCCGGAGGCATT 120

Qy   1979 cctggaggcagcagatattcctccgagtagccaccccgcagaaggcgtgcgattcttcca 2038
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCTGGAGGCAGCAGATATTCCTCCGAGTAGCCACCCCGCAGAAGGCGTGCGATTCTTCCA 180

Qy   2039 gcagatatgaagattattcagagctgggagagcttcccccacgatctcctttagaaccag 2098
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    181 GCAGATATGAAGATTATTCAGAGCTGGGAGAGCTTCCCCCACGATCTCCTTTAGAACCAG 240

Qy   2099 tttgtgaagatgggccctttggccccccaccagaggaaaagaaaaggacatctcgtgagc 2158
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TTTGTGAAGATGGGCCCTTTGGCCCCCCACCAGAGGAAAAGAAAAGGACATCTCGTGAGC 300

Qy   2159 tccgagagctgtggcaaaaggctattcttcaacagatactgctgcttagaatggagaagg 2218
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TCCGAGAGCTGTGGCAAAAGGCTATTCTTCAACAGATACTGCTGCTTAGAATGGAGAAGG 360

Qy   2219 aaaatcagaagctccaagcctctgaaaatgatttgctgaacaagcgcctgaagctcgatt 2278
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AAAATCAGAAGCTCCAAGCCTCTGAAAATGATTTGCTGAACAAGCGCCTGAAGCTCGATT 420

Qy   2279 atgaagaaattactccctgtcttaaagaagtaactacagtgtgggaaaagatgcttagca 2338
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ATGAAGAAATTACTCCCTGTCTTAAAGAAGTAACTACAGTGTGGGAAAAGATGCTTAGCA 480

Qy   2339 ctccaggaagatcaaaaattaagtttgacatggaaaaaatgcactcggctgttgggcaag 2398
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CTCCAGGAAGATCAAAAATTAAGTTTGACATGGAAAAAATGCACTCGGCTGTTGGGCAAG 540

Qy   2399 gtgtgccacgtcatcaccgaggtgaaatctggaaatttctagctgagcaattccaccctta 2458
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GTGTGCCACGTCATCACCGAGGTGAAATCTGGAAATTTCTAGCTGAGCAATTCCACCTTA 600

Qy   2459 aacaccagtttcccagcaaacagcagccaaaggatgtgccatacaaagaactcttaaagc 2518
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AACACCAGTTTCCCAGCAAACAGCAGCCAAAGGATGTGCCATACAAAGAACTCTTAAAGC 660

Qy   2519 agctgacttcccagcagcatgcgattcttattgaccttgggcgaacctttcctacacacc 2578
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    661 AGCTGACTTCCCAGCAGCATGCGATTCTTATTGACCTTGGGCGAACCTTTCCTACAAACC 720

Qy   2579 catacttctctgcccagcttggagcaggacagctatcgctttacaacattttgaaggcct 2638
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CATACTTCTCTGCCCAGCTTGGAGCAGGACAGCTATCGCTTTACAACATTTTGAAGGCCT 780

Qy   2639 actc 2642
           ||||
Db    781 ACTC 784


RESULT   5
BG759286
LOCUS       BG759286                 835 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602710975F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4851090 5',
            mRNA sequence.
ACCESSION   BG759286
VERSION     BG759286.1  GI:14069939
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 835)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1693  row: f  column: 19
            High quality sequence stop: 766.
FEATURES             Location/Qualifiers
     source          1. .835
                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:4851090"
                     /clone_lib="NIH_MGC_48"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      220 a    230 c    214 g    171 t
ORIGIN


  Query Match             20.9%;  Score 741.8;  DB 10;  Length 835;
  Best Local Similarity   98.8%;  Pred. No. 1.9e-174;
  Matches  768;  Conservative    0;  Mismatches    7;  Indels    2;  Gaps    2;

Qy   1591 gatagctccctgtctagtacattaagtaacaccagcaaagagccatctgtgtgtgaaaag 1650
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GATAGCTCCCTGTCTAGTACATTAAGTAACACCAGCAAAGAGCCATCTGTGTGTGAAAAG 60

Qy   1651 gaggccttgcccatctctgagagctcctttaagctcctcggctcctcggaggacctgtcc 1710
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GAGGCCTTGCCCATCTCTGAGAGCTCCTTTAAGCTCCTCGGCTCCTCGGAGGACCTGTCC 120

Qy   1711 agtgactcggagagtcatctcccagaagagccagctccgctgtcgccccagcaggccttc 1770
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGTGACTCGGAGAGTCATCTCCCAGAAGAGCCAGCTCCGCTGTCGCCCCAGCAGGCCTTC 180

Qy   1771 aggaggcgagcaaacaccctgagtcacttccccatcgaatgccaggaacctccacaacct 1830
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AGGAGGCGAGCAAACACCCTGAGTCACTTCCCCATCGAATGCCAGGAACCTCCACAACCT 240

Qy   1831 gcccgggggtccccgggggtttcgcaaaggaaacttatgaggtatcactcagtgagcaca 1890
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GCCCGGGGGTCCCCGGGGGTTTCGCAAAGGAAACTTATGAGGTATCACTCAGTGAGCACA 300

Qy   1891 gagacgcctcatgaacgaaaggactttgaatccaaagcaaaccatcttggtgattctggt 1950
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GAGACGCCTCATGAACGAAAGGACTTTGAATCCAAAGCAAACCATCTTGGTGATTCTGGT 360

Qy   1951 gggactcctgtgaagacccggaggcattcctggaggcagcagatattcctccgagtagcc 2010
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GGGACTCCTGTGAAGACCCGGAGGCATTCCTGGAGGCAGCAGATATTCCTCCGAGTAGCC 420

Qy   2011 accccgcagaaggcgtgcgattcttccagcagatatgaagattattcagagctgggagag 2070
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ACCCCGCAGAAGGCGTGCGATTCTTCCAGCAGATATGAAGATTATTCAGAGCTGGGAGAG 480

Qy   2071 cttcccccacgatctccttttagaaccagtttgtgaagatgggccctttggcccccccacca 2130
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CTTCCCCCACGATCTCCTTTAGAACCAGTTTGTGAAGATGGGCCCTTTGGCCCCCCCACCA 540

Qy   2131 gaggaaaagaaaaggacatctcgtgagctccgagagctgtggcaaaaggctattcttcaa 2190
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAGGAAAAGAAAAGGACATCTCGTGAGCTCCGAGAGCTGTGGCAAAAGGCTATTCTTCAA 600

Qy   2191 cagatactgctgcttagaatggagaaggaaaatcagaagctccaagcctctgaaaatgat 2250
           ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db    601 CAGATACTGCTGCTTAGAATGGAGAAGGAAAATCAGAAGCTCCAAGCCTCTGAACATGAT 660

Qy   2251 ttgctgaacaagcgcctgaagctcgattatgaagaaattactccctgtcttaaagaagta 2310
           |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db    661 TTGCTGAACAAGCGCCTGAAGCTCGATTATGACGAAATTACTCCCTGTCTTAAAGAAGTA 720

Qy   2311 actacagtgt-gggaaaagatgctta-gcactccaggaagatcaaaaattaagtttg 2365
           |||||||||| ||||| ||||||||| |||||||||||||||||| ||| | ||| |
Db    721 ACTACAGTGTGGGGAACAGATGCTTAGGCACTCCAGGAAGATCAACAATCAGGTTCG 777
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RESULT   6
BG746377
LOCUS       BG746377                 800 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602703644F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4856891 5',
            mRNA sequence.
ACCESSION   BG746377
VERSION     BG746377.1  GI:14057030
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 800)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: NIH Intramural Sequencing Center
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1708  row: h  column: 12
            High quality sequence stop: 762.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:4856891"
                     /clone_lib="NIH_MGC_15"
                     /tissue_type="adenocarcinoma cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)"
BASE COUNT      213 a    218 c    203 g    166 t
ORIGIN


  Query Match             20.8%;  Score 738.8;  DB 10;  Length 800;
  Best Local Similarity   98.6%;  Pred. No. 1.1e-173;
  Matches  787;  Conservative    0;  Mismatches    7;  Indels    4;  Gaps    4;

Qy   1502 agagatctttaacagagtctttagaaagtattttgtcccggggtaataaagccagaggcc 1561
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 AGAGATCTTTAACAGAGTCTTTAGAAAGTATTTTGTCCCGGGGTAATAAAGCCAGAGGCC 61

Qy   1562 tgcaggaacactccatcagtgtggatctggatagctccctgtctagtacattaagtaaca 1621
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 TGCAGGAACACTCCATCAGTGTGGATCTGGATAGCTCCCTGTCTAGTACATTAAGTAACA 121

Qy   1622 ccagcaaagagccatctgtgtgtgaaaaggaggccttgcccatctctgagagctccttta 1681
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    122 CCAGCAAAGAGCCATCTGTGTGTGAAAAGGAGGCCTTGCCCATCTCTGAGAGCTCCTTTA 181

Qy   1682 agctcctcggctcctcggaggacctgtccagtgactcggagagtcatctcccagaagagc 1741
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    182 AGCTCCTCGGCTCCTCGGAGGACCTGTCCAGTGACTCGGAGAGTCATCTCCCAGAAGAGC 241

Qy   1742 cagctccgctgtcgccccagcaggccttcaggaggcgagcaaacaccctgagtcacttcc 1801
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    242 CAGCTCCGCTGTCGCCCCAGCAGGCCTTCAGGAGGCGAGCAAACACCCTGAGTCACTTCC 301
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Qy   1802 ccatcgaatgccaggaacctccacaacctgcccgggggtccccgggggtttcgcaaagga 1861
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    302 CCATCGAATGCCAGGAACCTCCACAACCTGCCCGGGGGTCCCCGGGGGTTTCGCAAAGGA 361

Qy   1862 aacttatgaggtatcactcagtgagcacagagacgcctcatgaacgaaaggactttgaat 1921
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    362 AACTTATGAGGTATCACTCAGTGAGCACAGAGACGCCTCATGAACGAAAGGACTTTGAAT 421

Qy   1922 ccaaagcaaaccatcttggtgattctggtgggactcctgtgaagacccggaggcattcct 1981
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    422 CCAAAGCAAACCATCTTGGTGATTCTGGTGGGACTCCTGTGAAGACCCGGAGGCATTCCT 481

Qy   1982 ggaggcagcagatattcctccgagtagccaccccgcagaaggcgtgcgattcttccagca 2041
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    482 GGAGGCAGCAGATATTCCTCCGAGTAGCCACCCCGCAGAAGGCGTGCGATTCTTCCAGCA 541

Qy   2042 g-atatgaagattattcagagctgggagagcttcccccacgatctcctttagaaccagtt 2100
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    542 GCATATGAAGATTATTCAGAGCTGGGAGAGCTTCCCCCACGATCTCCTTTAGAACCAGTT 601

Qy   2101 tgtgaa-gatgggccctttggcccccccaccagaggaaaagaaaaggacatctcgtgagct 2159
          |||||| ||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db    602 TGTGAACGATGGGCCCTTTGGCCCCCCACCAGAGGAACAGAAAAGGACATCTCGTGAGCT 661

Qy   2160 ccgagagctgtggcaaaaggctattcttcaacagatactgctgcttagaatgga-gaagg 2218
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db    662 CCGAGAGCTGTGGCAAAAGGCTATTCTTCAACAGATACTGCTGCTTAGAATGGACGAAGG 721

Qy   2219 aaaatcagaagctccaagcctctgaaaatgatttgctg-aacaagcgcctgaagctcgat 2277
          ||||||||||||||||| |||||| |||||||||| ||| ||||||||||||||||||||
Db    722 CAAATCAGAAGCTCCAAGCTTCTGAACATGATTTGCTGAAACCAGCGCCTGAAGCTCGAT 781

Qy   2278 tatgaagaaattactccc 2295
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Db    782 CATGAAGAAATCACTCCC 799
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RESULT 7
BM476629
LOCUS BM476629 1121 bp mRNA linear EST 05-FEB-2002
DEFINITION AGENCOURT_6476337 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:5553589 5', mRNA sequence.
ACCESSION BM476629
VERSION BM476629.1 GI:18525671
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1121)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12270 row: m column: 14
High quality sequence start: 6
High quality sequence stop: 636.
FEATURES Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5553589"
/clone_lib="NIH_MGC_85"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
BASE COUNT 312 a 277 c 280 g 251 t 1 others
ORIGIN

Query Match 20.7%; Score 737.4; DB 10; Length 1121;
Best Local Similarity 96.1%; Pred. No. 2.8e-173;
Matches 799; Conservative 0; Mismatches 26; Indels 6; Gaps 4;

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Qy    830 acaatattgtgcagcccacagatatcgaggaaaatcgaactatgctcttcacgattggcc 889
          || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     31 ACTATATTGTGCAGCCCACAGATATCGAGGAAAATCGAACTATGCTCTTCACGATTGGCC 90

Qy    890 agtctgaagtttacctcatcagtcctgacaccaaaaaaaatagcat-tggagaaaaatttt 948
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db     91 AGTCTGAAGTTTACCTCATCAGTCCTGACACCAAAAAAATAGCATNTGGAGAAAAATTTT 150

Qy    949 aaggagatatccttttgctctcagggcatcagacacgtggaccactttgggtttatctgt 1008
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    151 AAGGAGATATCCTTTTGCTCTCAGGGCATCAGACACGTGGACCACTTTGGGTTTATCTGT 210

Qy   1009 cgggagtcttccggaggtggcggctttcattttgtctgttacgtgtttcagtgcacaaat 1068
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    211 CGGGAGTCTTCCGGAGGTGGCGGCTTTCATTTTGTCTGTTACGTGTTTCAGTGCACAAAT 270

Qy   1069 gaggctctggttgatgaaattatgatgaccctgaaacaggccttcacggtggccgcagtg 1128
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    271 GAGGCTCTGGTTGATGAAATTATGATGACCCTGAAACAGGCCTTCACGGTGGCCGCAGTG 330

Qy   1129 cagcagacagctaaggcgccagcccagctgtgtgagggctgccccctgcaaagcctgcac 1188
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    331 CAGCAGACAGCTAAGGCGCCAGCCCAGCTGTGTGAGGGCTGCCCCCTGCAAAGCCTGCAC 390

Qy   1189 aagctctgtgagaggatagagggaatgaattcttccaaaacaaaactagaactgcaaaag 1248
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    391 AAGCTCTGTGAGAGGATAGAGGGAATGAATTCTTCCAAAACAAAACTAGAACTGCAAAAG 450

Qy   1249 cacctgacgacattaaccaatcaggagcaggcgactatttttgaagaggttcagaaattg 1308
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    451 CACCTGACGACATTAACCAATCAGGAGCAGGCGACTATTTTTGAAGAGGTTCAGAAATTG 510

Qy   1309 agaccgagaaatgagcagcgagagaatgaattgattatttctttttctgagatgtttatat 1368
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    511 AGACCGAGAAATGAGCAGCGAGAGAATGAATTGATTATTTCTTTTCTGAGATGTTTATAT 570

Qy   1369 gaagagaaacagaaagaacacatccatattggggagatgaagcagacatcgcagatggca 1428
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    571 GAAGAGAAACAGAAAGAACACATCCATATTGGGGAGATGAAGCAGACATCGCAGATGGCA 630

Qy   1429 gcagagaatattggaagtgaattaccacccagtgccactcgatttaggctagatatgctg 1488
          |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db    631 GCAGAGAATATTGGAAGTGAATTACCACCCAGTGCCCCTCGATTTAGGCTAGATATGCTG 690

Qy   1489 aaaaacaaagcaaagagatctttaacagagtctttagaaagtattttgtcccggggtaat 1548
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    691 AAAAACAAAGCAAAGAGATCTTTAACAGAGTCTTTAGAAAGTATTTTGTCCCGGGGTAAT 750

Qy   1549 aaagccagaggcctgcaggaacactccatcagtgt---ggatctggatagctcccct-gtc 1604
          |||||||||||||||||| |  |  |      ||   ||||||||||||||||||| |||
Db    751 AAAGCCAGAGGCCTGCAGGGAACCCTCCATCCCGTGTGGGATCTGGATAGCTCCCTGGTC 810

Qy   1605 tagtaca-ttaagtaacaccagcaaagagccatctgtgtgtgaaaaggagg 1654
          ||||||| |||||||||||||||||     |     |||||| |||   ||
Db    811 TAGTACATTTAAGTAACACCAGCAAAAGAGCCATCCTGTGTGTAAAAAGGG 861
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RESULT 8
BM460573
LOCUS BM460573 1109 bp mRNA linear EST 05-FEB-2002

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DEFINITION  AGENCOURT_6421241 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5531908
            5', mRNA sequence.
ACCESSION   BM460573
VERSION     BM460573.1  GI:18509613
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1109)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12214  row: f  column: 05
            High quality sequence stop: 630.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:5531908"
                     /clone_lib="NIH_MGC_71"
                     /tissue_type="leiomyosarcoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 2.1 kb.  "
BASE COUNT      301 a    311 c    258 g    239 t
ORIGIN
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  Query Match             20.5%;  Score 729.8;  DB 10;  Length 1109;
  Best Local Similarity   97.5%;  Pred. No. 2.2e-171;
  Matches  773;  Conservative    0;  Mismatches   17;  Indels    3;  Gaps    3;

Qy   1340 tgattatttcttttctgagatgtttatatgaagagaaacagaaagaacacatccatattg 1399
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     13 TGATTATTTCTTTTCTGAGATGTTTATATGAAGAGAAACAGAAAGAACACATCCATATTG 72

Qy   1400 gggagatgaagcagacatcgcagatggcagcagagaatattggaagtgaattaccaccca 1459
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     73 GGGAGATGAAGCAGACATCGCAGATGGCAGCAGAGAATATTGGAAGTGAATTACCACCCA 132

Qy   1460 gtgccactcgatttaggctagatatgctgaaaaacaaagcaaagagatctttaacagagt 1519
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    133 GTGCCACTCGATTTAGGCTAGATATGCTGAAAAACAAAGCAAAGAGATCTTTAACAGAGT 192

Qy   1520 ctttagaaagtattttgtcccggggtaataaagccagaggcctgcaggaacactccatca 1579
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    193 CTTTAGAAAGTATTTTGTCCCGGGGTAATAAAGCCAGAGGCCTGCAGGAACACTCCATCA 252

Qy   1580 gtgtggatctggatagctccctgtctagtacattaagtaacaccagcaaagagccatctg 1639
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    253 GTGTGGATCTGGATAGCTCCCTGTCTAGTACATTAAGTAACACCAGCAAAGAGCCATCTG 312

Qy   1640 tgtgtgaaaaggaggccttgcccatctctgagagctcctttaagctcctcggctcctcgg 1699
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Db    313 TGTGTGAAAAGGAGGCCTTGCCCATCTCTGAGAGCTCCTTTAAGCTCCTCGGCTCCTCGG 372

Qy   1700 aggacctgtccagtgactcggagagtcatctcccagaagagccagctccgctgtcgcccc 1759
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Db    373 AGGACCTGTCCAGTGACTCGGAGAGTCATCTCCCAGAAGAGCCAGCTCCGCTGTCGCCCC 432

Qy   1760 agcaggccttcaggaggcgagcaaacaccctgagtcacttccccatcgaatgccaggaac 1819
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    433 AGCAGGCCTTCAGGAGGCGAGCAAACACCCTGAGTCACTTCCCCATCGAATGCCAGGAAC 492

Qy   1820 ctccacaacctgcccgggggtccccgggggtttcgcaaaggaaacttatgaggtatcact 1879
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    493 CTCCACAACCTGCCCGGGGGTCCCCGGGGGTTTCGCAAAGGAAACTTATGAGGTATCACT 552

Qy   1880 cagtgagcacagagacgcctcatgaacgaaaggactttgaatccaaagcaaaccatcttg 1939
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    553 CAGTGAGCACAGAGACGCCTCATGAACGAAAGGACTTTGAATCCAAAGCAAACCATCTTG 612

Qy   1940 gtgattctggtgggactcctgtgaagacccggaggcattcctggaggcagcagatattcc 1999
          |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db    613 GTGATTCTGGTGGGACTCCTGTGAAGACCCCGGAGCATTCCTGGAGGCAGCAGATATTCC 672

Qy   2000 tccgagtagccaccccgcagaaggcgtgcgattcttccagcagatatgaagattattcag 2059
          ||||||||||||||||||||||||||||| ||||||||||||||||||||| |||||||| |
Db    673 TCCGAGTAGCCACCCCGCAGAAGGCGGGCGATTCTTCCAGCAGATATGGAGATTATTCCG 732

Qy   2060 agct-gggagagcttcccccacgatc-tcctttagaaccagtttgt-gaagatgggccct 2116
          |||| |||||||||||||| | | | ||| |||||||||||||| ||||||||| ||
Db    733 AGCTGGGGAGAGCTTCCCCCCCCAACTTCCCTTAGAACCAGTTTGTGGAAGATGGGGCCC 792

Qy   2117 ttggccccccacc 2129
          || |  | || ||
Db    793 TTTGGGCGCCTCC 805
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RESULT   9
BE299948
LOCUS       BE299948                952 bp    mRNA    linear   EST 20-JUL-2000
DEFINITION  600944494F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960782 5',
            mRNA sequence.
ACCESSION   BE299948
VERSION     BE299948.1  GI:9183696
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 952)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM54  row: k  column: 23
            High quality sequence stop: 709.
FEATURES             Location/Qualifiers
     source          1. .952
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:2960782"
                     /clone_lib="NIH_MGC_17"
                     /tissue_type="rhabdomyosarcoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
                     Site_2: XhoI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G).  Size-selected >500bp
                     for average insert size 1.8kb.  Library constructed by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      249 a    240 c    250 g    212 t      1 others
ORIGIN
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  Query Match            20.3%;  Score 722.2;  DB 10;  Length 952;
  Best Local Similarity  97.2%;  Pred. No. 1.7e-169;
  Matches  766;  Conservative    0;  Mismatches   19;  Indels    3;  Gaps    3;

Qy   1879 tcagtgagcacagagacgcctcatgaacgaaaggactttgaatccaaagcaaaccatctt 1938
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TCAGTGAGCACAGAGACGCCTCATGAACGAAAGGACTTTGAATCCAAAGCAAACCATCTT 60

Qy   1939 ggtgattctggtgggactcctgtgaagacccggaggcattcctggaggcagcagatattc 1998
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GGTGATTCTGGTGGGACTCCTGTGAAGACCCGGAGGCATTCCTGGAGGCAGCAGATATTC 120

Qy   1999 ctccgagtagccaccccgcagaaggcgtgcgattcttccagcagatatgaagattattca 2058
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CTCCGAGTAGCCACCCCGCAGAAGGCGTGCGATTCTTCCAGCAGATATGAAGATTATTCA 180

Qy   2059 gagctgggagagcttcccccacgatctcctttagaaccagtttgtgaagatgggccctttt 2118
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GAGCTGGGAGAGCTTCCCCCACGATCTCCTTTAGAACCAGTTTGTGAAGATGGGCCCTTT 240

Qy   2119 ggcccccccaccagaggaaaagaaaaggacatctcgtgagctccgagagctgtggcaaaag 2178
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GGCCCCCCACCAGAGGAAAAGAAAAGGACATCTCGTGAGCTCCGAGAGCTGTGGCAAAAG 300

Qy   2179 gctattcttcaacagatactgctgcttagaatggagaaggaaaatcagaagctccaagcc 2238
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GCTATTCTTCAACAGATACTGCTGCTTAGAATGGAGAAGGAAAATCAGAAGCTCCAAGCC 360

Qy   2239 tctgaaaatgatttgctgaacaagcgcctgaagctcgattatgaagaaattactccctgt 2298
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TCTGAAAATGATTTGCTGAACAAGCGCCTGAAGCTCGATTATGAAGAAATTACTCCCTGT 420

Qy   2299 cttaaagaagtaactacagtgtgggaaaagatgcttagcactccaggaagatcaaaaatt 2358
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Db    421 CTTAAAGAAGTAACTACAGTGTGGGAAAAGATGCTTAGCACTCCAGGAAGATCAAAAATT 480

Qy   2359 aagtttgacatggaaaaaatgcactcggctgttgggcaaggtgtgccacgtcatcaccga 2418
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Db    481 AAGTTTGACATGGAAAAAATGCACTCGGCTG-TGGGCAAGGTGTGCCACGTCATCACCGA 539

Qy   2419 ggtgaaatctggaaatttctagctgagcaattccaccttaaacaccagtttcccagcaaa 2478
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Db    540 GGTGAAATCTGGAAATTTCTAGCTGAGCAATTCCACCTTAAACACCAGTTTCCCAGCAAA 599

Qy   2479 cagcagccaaaggatgtgccatacaaagaactcttaaagcagctgacttcccagcagcat 2538
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    600 CAGCAGCCAAAGGATGTGCCATACAAAGAACTCTTAAAGCAGCTGACTTCCCAGCAGCAT 659

Qy   2539 gcgattctta-ttgaccttgggcgaaccttcctacacacccatacttctctgcccagct 2597
          |||||||||| |||||| ||||||||||||||||||||||||||||||||| | |||||
Db    660 GCGATTCTTATTTGACCTGNGGCGAACCTTTCCTACACACCCATACTTCTCTGCCCAG-T 718

Qy   2598 tggagcaggacagctatcgctttacaacattttgaaggcctactcacttctagaccagga 2657
          |||||||||||||||||||||||||||||||   ||| ||||||   |      |||||
Db    719 TGGAGCAGGACAGCTATCGCTTTACAACATTTGTGAGGGCTACTCCACTTCTAGACAGGA 778

Qy   2658 agtgggat 2665
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Db    779 GTGGGTAT 786


RESULT  10
BI907513
LOCUS       BI907513                838 bp    mRNA    linear   EST 16-OCT-2001
DEFINITION  603065640F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5214945 5',
            mRNA sequence.
ACCESSION   BI907513
VERSION     BI907513.1  GI:16170347
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 838)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11539  row: o  column: 10
            High quality sequence start: 4
            High quality sequence stop: 780.
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                     /tissue_type="leukocyte"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
                     (destroyed); RNA source leukocytes from anonymous pool of
                     non-activated  adult donors.  Library is oligo-dT primed
                     and directionally cloned  (EcoRV site is destroyed upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     1.2-3.3 kb.  Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen).  Research Genetics tracking code 027. Note:
                     this is a NIH_MGC Library."
BASE COUNT      237 a    199 c    191 g    211 t
ORIGIN


  Query Match            20.1%;  Score 713.8;  DB 10;  Length 838;
  Best Local Similarity  97.0%;  Pred. No. 2e-167;
  Matches  812;  Conservative    0;  Mismatches   17;  Indels    8;  Gaps    8;

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Db      9 GAAGCTCCAAGCCTCTGAAAATGATTTGCTGAACAAGCGCCTGAAGCTCGATTATGAAGA 68

Qy   2286 aattactccctgtcttaaagaagtaactacagtgtgggaaaagatgcttagcactccagg 2345
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Db     69 AATTACTCCCTGTCTTAAAGAAGTAACTACAGTGTGGGAAAAGATGCTTAGCACTCCAGG 128

Qy   2346 aagatcaaaaattaagtttgacatggaaaaaatgcactcggctgttgggcaaggtgtgcc 2405
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    129 AAGATCAAAAATTAAGTTTGACATGGAAAAAATGCACTCGGCTGTTGGGCAAGGTGTGCC 188

Qy   2406 acgtcatcaccgaggtgaaatctggaaatttctagctgagcaattccaccttaaacacca 2465
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    189 ACGTCATCACCGAGGTGAAATCTGGAAATTTCTAGCTGAGCAATTCCACCTTAAACACCA 248

Qy   2466 gtttcccagcaaacagcagccaaaggatgtgccatacaaagaactcttaaagcagctgac 2525
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    249 GTTTCCCAGCAAACAGCAGCCAAAGGATGTGCCATACAAAGAACTCTTAAAGCAGCTGAC 308

Qy   2526 ttcccagcagcatgcgattcttattgaccttgggcgaaccttcctacacacccatactt 2585
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Db    309 TTCCCAGCAGCATGCGATTCTTA-TGACCTTGGGCGAACCTTTCCTACACACCCATACTT 367

Qy   2586 ctctgcccagcttggagcaggacagctatcgctttacaacattttgaaggcctactcact 2645
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Db    368 CTCTGCCCAGCTTGGAGCAGGACAGCTATCGCTTTACAACA-TTTGAAGGCCTACTCACT 426

Qy   2646 tctagaccaggaagtgggatattgccaaggtctcagctttgtagcaggcattttgcttct 2705
          |||||||||||||||||||| |||||||||||||||| |||||||||| |||||||||
Db    427 TCTAGACCAGGAAGTGGGATA-TGCCAAGGTCTCAGC-TTGTAGCAGGCA-TTTGCTTCT 483
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Qy   2706 tcatatgagtgaggaagaggcgtttaaaatgctcaagtttctgatgtttgacatggggct 2765
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Db    484 TCATATGAGTGAGGAAGAGGCGTTTAAAATGCTCAAGTTTCTGATG-TTGACATGGGGCT 542

Qy   2766 gcggaaacagtatcggccagacatgattatttacagatccagatgtaccagctctcgag 2825
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    543 GCGGAAACAGTATCGGCCAGACATGATTATTTTACAGATCCAGATGTACCAGCTCTCGAG 602

Qy   2826 gttgcttcatgattaccacagagacctctacaatcacctggaggagcacgagatcggccc 2885
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    603 GTTGCTTCATGATTACCACAGAGACCTCTACAATCACCTGGAGGAGCACGAGATCGGCCC 662

Qy   2886 cagcctctacgctg-ccccctggttcctcaccatgtttgcctcacagttcccgctgggat 2944
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    663 CAGCCTCTACGCTGCCCCCCTGGTTCCTCACCATGTTTGCCTCACAGTTCCCGCTGGGAT 722

Qy   2945 tcgtagccagagtctttgatatgatttttcttcagggaacagaggtcatatttaaagtgg 3004
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Db    723 TCGTAGCCAGAGTCTTTGATATGATTTTTCTTCAGGGAACAGAGGTCATATTTAAAGTGG 782

Qy   3005 ctttaagtctgttgggaagccataagcccttgattctgcagcatgaaaacctagaaa 3061
           ||||| ||   ||||||| |||||||||   |         ||||||||||||||
Db    783 -TTTAAATCCTGTGGGAAGGCATAAGCCCTGATTCTGCAGCATTGAAAACCTAGAAA 838


RESULT 11
BG120498
LOCUS       BG120498                807 bp    mRNA    linear   EST 30-JAN-2001
DEFINITION  602346815F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4441923 5',
            mRNA sequence.
ACCESSION   BG120498
VERSION     BG120498.1  GI:12614007
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 807)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10213  row: n  column: 04
            High quality sequence stop: 682.
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                     /clone_lib="NIH_MGC_90"
                     /tissue_type="adenocarcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 1.7 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
BASE COUNT      231 a    197 c    189 g    190 t
ORIGIN


  Query Match             19.8%;  Score 705;  DB 10;  Length 807;
  Best Local Similarity   96.1%;  Pred. No. 3.1e-165;
  Matches  766;  Conservative    0;  Mismatches   25;  Indels    6;  Gaps    4;
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Qy   1992 gatattcctccgagtagccaccccgcagaaggcgtgcgattcttccagcagatatgaaga 2051
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Db      1 GATATTCCTCCGAGTAGCCACCCCGCAGAAGGCGTGCGATTCTTCCAGCAGATATGAAGA 60

Qy   2052 ttattcagagctgggagagcttcccccacgatctcctttagaaccagtttgtgaagatgg 2111
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TTATTCAGAGCTGGGAGAGCTTCCCCCACGATCTCCTTTAGAACCAGTTTGTGAAGATGG 120

Qy   2112 gccctttggcccccccaccagaggaaaagaaaaggacatctcgtgagctccgagagctgtg 2171
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Db    121 GCCCTTTGGCCCCCCACCAGAGGAAAAGAAAAGGACATCTCGTGAGCTCCGAGAGCTGTG 180

Qy   2172 gcaaaaggctattcttcaacagatactgctgcttagaatggagaaggaaaatcagaagct 2231
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GCAAAAGGCTATTCTTCAACAGATACTGCTGCTTAGAATGGAGAAGGAAAATCAGAAGCT 240

Qy   2232 ccaagcctctgaaaatgatttgctgaacaagcgcctgaagctcgattatgaagaaattac 2291
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Db    241 CCAAGCCTCTGAAAATGATTTGCTGAACAAGCGCCTGAAGCTCGATTATGAAGAAATTAC 300

Qy   2292 tccctgtcttaaagaagtaactacagtgtgggaaaagatgcttagcactccaggaagatc 2351
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TCCCTGTCTTAAAGAAGTAACTACAGTGTGGGAAAAGATGCTTAGCACTCCAGGAAGATC 360

Qy   2352 aaaaattaagtttgacatggaaaaaatgcactcggctgttgggcaaggtgtgccacgtca 2411
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Db    361 AAAAATTAAGTTTGACATGGAAAAAATGCACTCGGCTGTTGGGCAAGGTGTGCCACGTCA 420

Qy   2412 tcaccgaggtgaaatctggaaatttctagctgagcaattccaccttaaacaccagtttcc 2471
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Db    421 TCACCGAGGTGAAATCTGGAAATTTCTAGCTGAGCAATTCCACCTTAAACACCAGTTTCC 480

Qy   2472 cagcaaacagcagccaaaggatgtgccatacaaagaactcttaaagcagctgacttccca 2531
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Db    481 CAGCAAACAGCAGCCAAAGGATGTGCCATACAAAGAACTCTTAAAGCAGCTGACTTCCCA 540

Qy   2532 gcagcatgcgattcttattgaccttgggcgaacctttcctacaca-cccatacttctctg 2590
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Db    541 GCAGCATGCGATTCTTATTGACCTTGGGCGAACCTTTCCTACACAGCCCATACTTCTCTG 600

Qy   2591 cccagcttggagcaggacagctatcgctttacaacattttgaaggcctactcacttctag 2650
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Db    601 CCCAGCTTGGAGCAGGACAGCTATCGCTTTACAACATTTTGAAGGCCTACTCACTTCTAG 660

Qy   2651 accaggaagtgggatattgcc--aaggtctcagcttt-gtagcaggcattttgcttcttc 2707
          |||||||||||||||||||  |||   |||||||| || |||||| | ||||||| ||
Db    661 ACCAGGAAGTGGGATATTGCCCAAAGTCTTCAGCTTTGGTGGCAGGCCTCTTGCTTCCTC 720

Qy   2708 atatgagtgaggaagaggcgtttaaaatgctcaagtttctgatgtttgacatggggctgc 2767
          |||||||||| |||||||||||| |||     ||   ||| ||||||||||||||| |
Db    721 ATATGAGTGACGAAGAGGCGTTAAAATGCTCCA--GTTCCGATGTTTGACATGGGCCGCG 778

Qy   2768 ggaaacagtatcggcca 2784
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Db    779 GGAACCAGTTCGGGCAA 795


RESULT 12
BM014940
LOCUS       BM014940                832 bp    mRNA    linear   EST 30-OCT-2001
DEFINITION  603640877F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5416818 5',
            mRNA sequence.
ACCESSION   BM014940
VERSION     BM014940.1  GI:16529294
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 832)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
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COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12063  row: j  column: 19
            High quality sequence stop: 811.
FEATURES             Location/Qualifiers
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                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 1.383 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
BASE COUNT      231 a    205 c    186 g    208 t      2 others
ORIGIN


  Query Match             19.7%;  Score 701;  DB 10;  Length 832;
  Best Local Similarity   97.5%;  Pred. No. 3.1e-164;
  Matches  785;  Conservative    0;  Mismatches   12;  Indels    8;  Gaps    7;

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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     29 CACGTCATCACCGAGGTGAAATCTGGAAATTTCTAGCTGAGCAATTCCACCTTAAACACC 88

Qy   2465 agtttcccagcaaacagcagccaaaggatgtgccatacaaagaactcttaaagcagctga 2524
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     89 AGTTTCCCAGCAAACAGCAGCCAAAGGATGTGCCATACAAAGAACTCTTAAAGCAGCTGA 148

Qy   2525 cttcccagcagcatgcgattcttattgaccttgggcgaacctttcctacacacccatact 2584
           |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    149 CTTCCCAGCAGCATGCGATTCTTA-TGACCTTGGGCGAACCTTTCCTACACACCCATACT 207

Qy   2585 tctctgcccagcttggagcaggacagctatcgctttacaacattttgaaggcctactcac 2644
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Db    208 TCTCTGCCCAGCTTGGAGCAGGACAGCTATCGCTTTACAACATTTTGAAGGCCTACTCAC 267

Qy   2645 ttctagaccaggaagtgggatattgccaaggtctcagctttgtagcaggcattttgcttc 2704
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Db    268 TTCTAGACCAGGAAGTGGGATATTGCCAAGGTCTCAGCTTTGTAGCAGGCATTNTGCTTC 327

Qy   2705 ttcatatgagtgaggaagaggcgtttaaaatgctcaagtttctgatgtttgacatggggc 2764
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Qy   2825 ggttgcttcatgattaccacagagacctctacaatcacctggaggagcacgagatcggcc 2884
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Db    448 GGTTGCTTCATGATTACCACAGAGACCTCTACAATCACCTGGAGGAGCACGAGATCGGCC 507

Qy   2885 ccagcctctacgctgccccctggttcctcaccatgtttgcctcacagttcccgctgggat 2944
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Db    508 CCAGCCTCTACGCTGCCCCCTGGTTCCTCACCATGTTTGCCTCACAGTTCCCGCTGGGAT 567

Qy   2945 tcgtagccagagtctttgatatgatttttcttcagggaacagaggtcatatttaa-agtg 3003
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Db    568 TCGTAGCCAGAGTCTTTGATATGATTTTTCTTCAGGGAACAGAGGTCATATTTAACAGTG 627

Qy   3004 gctttaagtctgttgggaagccataagcccttgattctgcagcatgaaaacctagaaacc 3063
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Db    628 GCTTTAAGTCTGNTGGGAAGCCATAAGCCCTTGATTCTGCAGCATGAAAACCTAGAAACC 687

Qy   3064 atagttgactttat-aaaaagcacgctacccaaccttggc-ttggtacagat-ggaaaag 3120
           |||||||||||||| |||||||||||| |||| |||||| |||||||||| ||||||| 
Db    688 ATAGTTGACTTTATAAAAAAGCACGCTAACCAAGCTTGGCTTTGGTACAGATGGGAAAAG 747

Qy   3121 accatcaatcaggtatttgaaatggacatcgctaaa--cagttacaagcttatgaagttg 3178
           |||||||||||||||||| |||||||||||| ||||     |   ||||||||||||||
Db    748 ACCATCAATCAGGTATTGGAAATGGACATCGGTAAAACAGTTACAAAGCTTATGAAGTTG 807

Qy   3179 agtacc-acgtccttcaagaagaac 3202
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Db    808 AGTACCAACGTCCTTCAAGAAGAAC 832


RESULT  13
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LOCUS       AL570425                851 bp    mRNA    linear   EST 16-FEB-2001
DEFINITION  AL570425 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI020YF02 5
            prime, mRNA sequence.
ACCESSION   AL570425
VERSION     AL570425.1  GI:12926720
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 851)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
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                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
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                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed by
                     Life Technologies. Contact : Feng Liang Life Technologies,
                     a division of Invitrogen 9800 Medical Center Drive
                     Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                     Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      240 a    214 c    220 g    174 t      3 others
ORIGIN


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Qy   2836 gattaccacagagacctctacaat--cacctggaggagcacgagatcggccccagcctct 2893
           |||||||||||||||||||||||     | ||||||||||||||||||||||||||||||
Db      1 GATTACCACAGAGACCTCTACAANTCACCTTGGAGGAGCACGAGATCGGCCCCAGCCTCT 60

Qy   2894 acgctgccccctggttcctcaccatgtttgcctcacagttcccgctgggattcgtagcca 2953
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Db     61 ACGCTGCCCCCTGGTTCCTCACCATGTTTGCCTCACAGTTCCCGCTGGGATTCGTAGCCA 120

Qy   2954 gagtctttgatatgatttttcttcagggaacagaggtcatatttaaagtggctttaagtc 3013
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Db    121 GAGTCTTTGATATGATTTTTCTTCAGGGAACAGAGGTCATATTTAAAGTGGCTTTAAGTC 180
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Qy   3014 tgttgggaagccataagcccttgattctgcagcatgaaaacctagaaaccatagttgact 3073
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Db    181 TGTTGGGAAGCCATAAGCCCTTGATTCTGCAGCATGAAAACCTAGAAACCATAGTTGACT 240

Qy   3074 ttataaaaagcacgctacccaaccttggcttggtacagatggaaaagaccatcaatcagg 3133
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TTATAAAAAGCACGCTACCCAACCTTGGCTTGGTACAGATGGAAAAGACCATCAATCAGG 300

Qy   3134 tatttgaaatggacatcgctaaacagttacaagcttatgaagttgagtaccacgtccttc 3193
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Db    301 TATTTGAAATGGACATCGCTAAACAGTTACAAGCTTATGAAGTTGAGTACCACGTCCTTC 360

Qy   3194 aagaagaacttatcgattcctctcctctcagtgacaaccaaagaatggataaattagaga 3253
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Db    361 AAGAAGAACTTATCGATTCCTCTCCTCTCAGTGACAACCAAAGAATGGATAAATTAGAGA 420

Qy   3254 aaaccaacagcagcttacgcaaacagaaccttgacctccttgaacagttgcaggtggcaa 3313
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Db    421 AAACCAACAGCAGCTTACGCAAACAGAACCTTGACCTCCTTGAACAGTTGCAGGTGGCAA 480

Qy   3314 atggtaggatccaaagccttgaggccaccattgagaagctcctgagcagtgagagcaagc 3373
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Db    481 ATGGTAGGATCCAAAGCCTTGAGGCCACCATTGAGAAGCTCCTGAGCAGTGAGAGCAAGC 540

Qy   3374 tgaagcaggccatgcttaccttagaactggagcggtcggccctgctgcagacggtggagg 3433
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Qy   3434 agctgcggcggcggagcgcagagcccagcgaccgggagcctgagtgcacgcagcccgagc 3493
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Db    601 AGCTGCGGCGGCGGA-SGCAGAGCCCAGCGACCGGGAGCCTGAGTGCACGCAGCCCGAGC 659

Qy   3494 ccacgggcgactgacagctctgcaggagagattgcaacaccatcccacactgtccaggcc 3553
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   3554 tt 3555
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Db    720 TT 721
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LOCUS       BE300005                754 bp    mRNA    linear   EST 20-JUL-2000
DEFINITION  600944594F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960783 5',
            mRNA sequence.
ACCESSION   BE300005
VERSION     BE300005.1  GI:9183753
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 754)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM54  row: k  column: 24
            High quality sequence start: 2
            High quality sequence stop: 753.
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                     /lab_host="DH10B (phage-resistant)"
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                     Site_2: XhoI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G).  Size-selected >500bp
                     for average insert size 1.8kb.  Library constructed by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      227 a    186 c    177 g    164 t
ORIGIN
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Qy   1878 ctcagtgagcacagagacgcctcatgaacgaaaggactttgaatccaaagcaaaccatct 1937
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Qy   1938 tggtgattctggtgggactcctgtgaagacccggaggcattcctggaggcagcagatatt 1997
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Qy   1998 cctccgagtagccacccccgcagaaggcgtgcgattcttccagcagatatgaagattattc 2057
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Db    120 CCTCCGAGTAGCCACCCCGCAGAAGGCGTGCGATTCTTCCAGCAGATATGAAGATTATTC 179

Qy   2058 agagctgggagagcttcccccacgatctcctttagaaccagtttgtgaagatgggccctt 2117
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Db    180 AGAGCTGGGAGAGCTTCCCCCACGATCTCCTTTAGAACCAG-TTGTGAAGATGGGCCC-T 237

Qy   2118 tggccccccaccagaggaaaagaaaaggacatctcgtgagctccgagagctgtggcaaaa 2177
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    238 TGGCCCCCCACCAGAGGAAAAGAAAAGGACATCTCGTGAGCTCCGAGAGCTGTGGCAAAA 297

Qy   2178 ggctattcttcaacagatactgctgcttagaatggagaaggaaaatcagaagctccaagc 2237
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Qy   2238 ctctgaaaatgatttgctgaacaagcgcctgaagctcgattatgaagaaattactccctg 2297
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Qy   2298 tcttaaagaagtaactacagtgtgggaaaagatgcttagcactccaggaagatcaaaaat 2357
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Db    417 TCTTAAAGAAGTAACTACAGTGTGGGAAAAGATGCTTAGCACTCCAGGAAGATCAAAAAT 476

Qy   2358 taagtttgacatggaaaaaatgcactcggctgttgggcaaggtgtgccacgtcatcaccg 2417
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Db    477 TAAGTTTGACATGGAAAAAATGCACTCGGCTGTTGGGCAAGGTGTGCCACGTCATCACCG 536

Qy   2418 aggtgaaatctggaaatttctagctgagcaattccaccttaaacaccagtttcccagcaa 2477
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Db    537 AGGTGAAATCTGGAAATTTCTAGCTGAGCAATTCCACCTTAAACACCAGTTTCCCAGCAA 596

Qy   2478 acagcagccaaaggatgtgccatacaaagaactcttaaagcagctgacttcccagcagca 2537
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Db    597 ACAGCAGCCAAAGGATGTGCCATACAAAGAACTCTTAAAGCAGCTGACTTCCCAGCAGCA 656

Qy   2538 tgcgattcttattgaccttgggcgaacctttcctacacacccatacttctctgcccagct 2597
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Db    657 TGCGATTCTTA-TGACCTTGGGCGAACCTTTCCTACACACCCATACTTCTCTGCCCAGCT 715

Qy   2598 tggagcaggacagctatcgctttacaacattttgaag 2634
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Db    716 TGGAGCAGGACAGCTATCGC-TTACAACATTTTGAGG 751
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RESULT 15

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BE561889
LOCUS       BE561889               892 bp    mRNA    linear   EST 15-AUG-2000
DEFINITION  601346094F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3678887 5',
            mRNA sequence.
ACCESSION   BE561889
VERSION     BE561889.1  GI:9805609
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 892)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM356  row: 1  column: 24
            High quality sequence start: 50
            High quality sequence stop: 758.
FEATURES             Location/Qualifiers
     source          1. .892
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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                     /clone_lib="NIH_MGC_8"
                     /tissue_type="Burkitt lymphoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      224 a    240 c    242 g    186 t
ORIGIN
```

Query Match 19.2%; Score 682.6; DB 10; Length 892;
Best Local Similarity 95.3%; Pred. No. 1.3e-159;
Matches 790; Conservative 0; Mismatches 29; Indels 10; Gaps 8;

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Qy   1628 aagagccatctgtgtgtgaaaaggaggccttgcccatctctgagagctcctttaagctcc 1687
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Db     63 AAGAGCCATCTGTGTGTGAAAAGGAGG-CTTGCCCATCTCTGAGAGCTCCTTTAAGCTCC 121

Qy   1688 tcggctcctcggaggacctgtccagtgactcggagagtcatctcccagaagagccagctc 1747
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    122 TCGGCTCCTCGGAGGACCTGTCCAGTGACTCGGAGAGTCATCTCCCAGAAGAGCCAGCTC 181

Qy   1748 cgctgtcgccccagcaggccttcaggaggcgagcaaacaccctgagtcactt-ccccatc 1806
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Qy   1807 gaatgccaggaacctccacaacctgcccgggggtccccgggggtttcgcaaaggaaactt 1866
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Qy   1867 atgaggtatcactcagtgagcacagagacgcctcatgaacgaaaggactttgaatccaaa 1926
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Qy   1987 cagcagatattcctccgagtagccaccccgcagaaggcgtgcgattcttccagcagatat 2046
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Qy   2047 gaagattattcagagctgggagagcttcccccacgatctcctttagaaccagtttgtgaa 2106
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2167 ctgtggcaaaaggctattcttcaacagatactgctgcttagaatggagaaggaaaatcag 2226
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Qy   2287 attactccctg-tcttaaagaagtaactacagtgtggga--aaagatgcttagcactcca 2343
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Qy   2344 ggaagatcaaaaattaagtttgacatggaaaaaatgcactcggctgttgggcaaggtgtg 2403
          ||||||||    ||| |||||| | |||  | ||||| ||||| |||||||| ||| | |
Db    782 GGAAGATC-CCCATTTAGTTTGGCCTGGTGACAATGC-CTCGGGTGTTGGGCCAGGGGGG 839

Qy   2404 ccacgtcatcaccgaggtgaaatctggaaatttctagctgagcaattcc 2452
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Search completed: September 9, 2002, 16:41:28
Job time: 9256 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: September 9, 2002, 19:18:41 ; Search time 706.85 Seconds
(without alignments)
8634.973 Million cell updates/sec

Title: US-09-762-311-4_COPY_176_3730
Perfect score: 3555
Sequence: 1 atggaaccaataacattcac.....tcccacactgtccaggcctt 3555

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3555	100.0	3983	21	AAZ50906	Human TBC-1 cDNA f
2	3555	100.0	3988	21	AAZ50907	Human TBC-1 cDNA f
3	3026.4	85.1	3326	22	AAI57854	Human polynucleoti
4	2940.2	82.7	3727	21	AAC77404	Human ORFX ORF2959
5	2833.8	79.7	3281	22	AAI59640	Human polynucleoti
6	2510.4	70.6	4039	19	AAV05886	Human Tbc-1 gene.
7	2112	59.4	2362	22	AAH18401	Human cDNA sequenc
8	1000.8	28.2	1422	22	AAS34787	cDNA encoding nove
9	999.4	28.1	2989	22	AAK94796	Human full-length
10	943.2	26.5	1269	22	AAS34785	cDNA encoding nove
11	785	22.1	883	22	AAH04450	Human cDNA clone (
12	574.2	16.2	849	22	AAK92006	Human cDNA 5'-end
13	574.2	16.2	849	22	AAK93666	Human cDNA clone r
14	422.6	11.9	17590	21	AAZ50904	Human TBC-1 partia
15	362	10.2	696	20	AAZ15229	Human gene express
16	306.2	8.6	5472	23	ABL02013	Drosophila melanog
17	284.4	8.0	99960	21	AAZ50905	Human TBC-1 partia
18	280	7.9	458	20	AAX40323	Human secreted pro
c 19	245.6	6.9	8105	23	ABL02012	Drosophila melanog
c 20	228.4	6.4	555	22	AAH09958	Human cDNA clone (
21	132.8	3.7	3691	22	AAF58616	Human RECAP polynu
22	132.8	3.7	4827	22	AAI59592	Human polynucleoti
23	132.8	3.7	5294	22	AAI57806	Human polynucleoti
24	128.8	3.6	3585	23	ABL12337	Drosophila melanog
25	123.8	3.5	154	23	AAS58636	cDNA #1312 encodin
26	119.4	3.4	2626	23	ABL18133	Drosophila melanog
27	119.4	3.4	7829	23	ABL18132	Drosophila melanog
28	108	3.0	2424	23	AAS71793	DNA encoding novel
29	83.8	2.4	1601	21	AAC33401	Arabidopsis thalia
c 30	79.6	2.2	6765	23	ABL12336	Drosophila melanog
31	78.4	2.2	300	20	AAZ13067	Human gene express
32	75.2	2.1	1492	21	AAC38750	Arabidopsis thalia
c 33	73.8	2.1	1140	21	AAZ97020	Human secreted pro
34	68.4	1.9	3342	22	AAF32789	Human secreted pro
35	68	1.9	2492	21	AAC78199	Human cancer assoc
36	65.2	1.8	1831	22	AAH64964	Human secreted pro
37	65	1.8	1117	22	AAI61302	Human polynucleoti
38	65	1.8	2035	22	AAF59600	Human cell cycle a
39	65	1.8	2482	22	AAI59516	Human polynucleoti
40	65	1.8	2666	22	AAH17866	Human cDNA sequenc
41	62.6	1.8	2531	23	ABL07359	Drosophila melanog
42	62.6	1.8	4661	23	ABL07358	Drosophila melanog
43	61.6	1.7	2801	22	AAF32643	Human cDNA encodin
c 44	61.6	1.7	2803	22	AAS27080	cDNA encoding nove
45	61.6	1.7	2903	22	AAK51641	Human polynucleoti

ALIGNMENTS

RESULT 1
AAZ50906
ID AAZ50906 standard; cDNA; 3983 BP.
XX
AC AAZ50906;
XX
DT 31-MAY-2000 (first entry)
XX
DE Human TBC-1 cDNA from first transcript.
XX
KW TBC-1; human; biallelic marker; chromosome 4; cell cycle regulator; SNP;
KW Single nucleotide polymorphism; tissue differentiation; prostate cancer;
KW linkage analysis; genetic map; detection; diagnosis; genotyping;
KW transgenic animal; screening; alternative splicing; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 5'UTR 1..170
FT /*tag= a
FT /note= "Spans through exon 1 and part of exon 2"
FT CDS 171..3677
FT /*tag= b
FT /product= "Human TBC-1 protein"
FT /note= "First transcription product"
FT 3'UTR 3726..3983
FT /*tag= c
FT polyA_signal 3942..3947
FT /*tag= d
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XX

PD 17-FEB-2000.
XX
PF 06-AUG-1999; 99WO-IB01444.
XX
PR 07-AUG-1998; 98US-0095653.
XX
PA (GEST) GENSET.
XX
PI Blumenfeld M, Bougueleret L, Chumakov I;
XX
DR WPI; 2000-205736/18.
DR P-PSDB; AAY45096.
XX
PT New isolated human TBC-1 nucleic acids, useful for developing products
PT for the diagnosis and treatment of disorders involving cell
PT proliferation, particularly prostate cancer -
XX
PS Claim 3; Page 150-155; 166pp; English.
XX
CC The present sequence is the cDNA encoding the first transcription
CC product of human TBC-1 protein, comprising exons 1-2 and A-L.
CC Alternative splicing events result in two mRNA molecules, due to
CC splicing at two distinct first exons, exon1 and exon 1bis. TBC-1 gene
CC is mapped to a candidate region of prostate cancer on chromosome 4.
CC TBC-1 gene is involved in the regulation of cell cycle and tissue
CC differentiation in mammals. An alteration of TBC-1 sequence may be
CC associated with a pathological condition, resulting in abnormal cell
CC proliferation leading to cancer, e.g. prostate cancer. The biallelic
CC markers can be used for generation of genetic maps, linkage analysis and
CC association studies. TBC-1 sequence can be used for detection,
CC diagnosis, genotyping, production of transgenic animals and screening
CC of compounds for use in therapy.
XX
SQ Sequence 3983 BP; 1090 A; 1007 C; 1007 G; 878 T; 1 other;

Query Match 100.0%; Score 3555; DB 21; Length 3983;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     61 tttggcctgcagctggtgggctccctgcctgtgcattccctgaccaccatgcccatgctg 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    121 ccctgggttgtggctgaggtgcgaagactcagcaggcagtccaccagaaaggaacctgta 180
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Qy    181 accaagcaagtccggctttgcgtttcaccctctggactgagatgtgaacctgagccaggg 240
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Qy    241 agaagtcaacagtgggatcccctgatctattccagcatctttgagtgcaagcctcagcgt 300
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Qy    301 gttcacaaactgattcacaacagtcatgacccaagttactttgcttgtctgattaaggaa 360
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Qy    361 gacgctgtccaccggcagagtatctgctatgtgttcaaagccgatgatcaaacaaaagtg 420
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Qy    421 cctgagatcatcagctccatccgtcaggcggggaagatcgcccggcaggaggagctgcac 480
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Qy    481 tgcccgtccgagttcgacgacacgttttccaagaagttcgaggtgctcttctgcggccgc 540
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Qy    541 gtgacggtggcgcacaagaaggctccgccggccctgatcgacgagtgcatcgagaagttc 600
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Qy    601 aatcacgtcagcggcagccgggggtccgagagcccccgccccaacccgccccatgccgcg 660
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Qy    661 cccacagggagccaggagcctgtgcgcaggcccatgcgcaagtccttctcccagcccggc 720
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Qy    721 ctgcgctcgctggcctttaggaaggagctgcaggatgggggcctccgaagcagcggcttc 780
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Qy   1141 aaggcgccagcccagctgtgtgagggctgccccctgcaaagcctgcacaagctctgtgag 1200
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Qy   1201 aggatagagggaatgaattcttccaaaacaaaactagaactgcaaaagcacctgacgaca 1260
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RESULT 2
AAZ50907
ID AAZ50907 standard; cDNA; 3988 BP.
XX
AC AAZ50907;
XX
DT 31-MAY-2000 (first entry)
XX
DE Human TBC-1 cDNA from second transcript.
XX
KW TBC-1; human; biallelic marker; chromosome 4; cell cycle regulator; SNP;

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KW   Single nucleotide polymorphism; tissue differentiation; prostate cancer;
KW   linkage analysis; genetic map; detection; diagnosis; genotyping;
KW   transgenic animal; screening; alternative splicing; ss.
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XX
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FT                   pancreas cDNA library"
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FT                   /*tag= c
FT                   /product= "Human TBC-1 protein"
FT                   /note= "Second transcription product"
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FT                   /*tag= d
FT   polyA_signal    3947..3952
FT                   /*tag= e
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XX
PR   07-AUG-1998;   98US-0095653.
XX
PA   (GEST ) GENSET.
XX
PI   Blumenfeld M,  Bougueleret L,  Chumakov I;
XX
DR   WPI; 2000-205736/18.
DR   P-PSDB; AAY45096.
XX
PT   New isolated human TBC-1 nucleic acids, useful for developing products
PT   for the diagnosis and treatment of disorders involving cell
PT   proliferation, particularly prostate cancer  -
XX
PS   Claim 4; Page 156-161; 166pp; English.
XX
CC   The present sequence is the cDNA encoding the second transcription
CC   product of human TBC-1 protein, comprising exons 1bis to 2 and A-L.
CC   Alternative splicing events result in two mRNA molecules, due to
CC   splicing at two distinct first exons, exon1 and exon 1bis. TBC-1 gene
CC   is mapped to a candidate region of prostate cancer on chromosome 4.
CC   TBC-1 gene is involved in the regulation of cell cycle and tissue
CC   differentiation in mammals. An alteration of TBC-1 sequence may be
CC   associated with a pathological condition, resulting in abnormal cell
CC   proliferation leading to cancer, e.g. prostate cancer. The biallelic
CC   markers can be used for generation of genetic maps, linkage analysis and
CC   association studies. TBC-1 sequence can be used for detection,
CC   diagnosis, genotyping, production of transgenic animals and screening
CC   of compounds for use in therapy.
XX
SQ   Sequence 3988 BP; 1107 A; 983 C; 1002 G; 896 T; 0 other;
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  Matches 3555;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 3
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AC AAI57854;
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DT 22-OCT-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 57.
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KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia; ss.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US34263.
XX
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0633450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR P-PSDB; AAM38698.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
PS Claim 1; SEQ ID NO 57; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
SQ Sequence 3326 BP; 924 A; 824 C; 843 G; 735 T; 0 other;

Query Match 85.1%; Score 3026.4; DB 22; Length 3326;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3030; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db   2863 accattgagaagctcctgagcagtgagagcaagctgaagcaggccatgcttaccttagaa 2922
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Db   2923 ctggagcggtcggccctgctgcagacggtggaggagctgcggcggcggagcgcagagccc 2982
Qy   3460 agcgaccgggagcctgagtgcacgcagcccgagcccacgggcgactgacagctctgcagg 3519
Db   2983 agcgaccgggagcctgagtgcacgcagcccgagcccacgggcgactgacagctctgcagg 3042
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Db   3043 agagattgcaacaccatcccacactgtccaggcctt 3078
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RESULT 4
AAC77404

ID AAC77404 standard; cDNA; 3727 BP.
XX
AC AAC77404;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human ORFX ORF2959 polynucleotide sequence SEQ ID NO:5917.
XX
KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cholesterol ester storage; systemic lupus erythematosus; infection;
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW thrombosis; contraceptive; ss.
XX
OS Homo sapiens.
XX
PN WO200058473-A2.
XX
PD 05-OCT-2000.
XX
PF 31-MAR-2000; 2000WO-US08621.
XX
PR 31-MAR-1999; 99US-0127607.
PR 02-APR-1999; 99US-0127636.
PR 05-APR-1999; 99US-0127728.
PR 30-MAR-2000; 2000US-0540763.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2000-602362/57.
DR P-PSDB; AAB43195.
XX
PT Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease -
XX
PS Claim 5; Page 5094-5096; 5507pp; English.
XX
CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC sequences have activities such as: cytostatic; hepatotropic; vulnerary;
CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
CC antidiabetic; hypotensive; dermatological; immunosuppressive;
CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
CC antithyroid; and antianaemic. The sequences can be used for determining
CC the presence of or predisposition to, or preventing or treating
CC pathological conditions associated with an ORFX-associated disorder. The
CC nucleic acids can be used to express ORFX proteins in gene therapy
CC vectors. The proteins and nucleic acids may be used to treat cancers,
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC graft vs host disease, cardiovascular disease, diabetes mellitus,
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
CC coagulation; to inhibit thrombosis; and as a contraceptive.
XX
SQ Sequence 3727 BP; 1031 A; 889 C; 931 G; 875 T; 1 other;

Query Match 82.7%; Score 2940.2; DB 21; Length 3727;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 3005; Conservative 0; Mismatches 13; Indels 7; Gaps 5;

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Qy   532 tgcggccgcgtgacggtggcgcacaagaaggctccgccggccctgatcgacgagtgcatc 591
Db     4 tgcggccgcgtgacggtggcgcacaagaaggctccgccggccctgatcgacgagtgcatc 63

Qy   592 gagaagttcaatcacgtcagcggcagccgggggtccgagagcccccgccccaacccgccc 651
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Qy   652 catgccgcgcccacagggagccaggagcctgtgcgcaggcccatgcgcaagtccttctcc 711
Db   124 catgccgcgcgccacagggagccaggacctgtgcgcaggcccatgcgcaagtccttctcc 183

Qy   712 cagcccggcctgcgctcgctggcctttaggaaggagctgcaggatgggggcctccgaagc 771
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Qy   772 agcggcttcttcagctccttcgaggagagcgacattgagaaccacctcattagcggacac 831
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Qy  1192 ctctgtgagaggatagagggaatgaattcttccaaaacaaaactagaactgcaaaagcac 1251
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Qy  1252 ctgacgacattaaccaatcaggagcaggcgactatttttgaagaggttcagaaattgaga 1311
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Qy  1312 ccgagaaatgagcagcgagagaatgaattgattatttctttttctgagatgtttatatgaa 1371
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Qy  1432 gagaatattggaagtgaattaccacccagtgccactcgatttaggctagatatgctgaaa 1491
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Qy  1492 aacaaagcaaagagatctttaacagagtctttagaaagtattttgtcccggggtaataaa 1551
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Qy   1552 gccagaggcctgcaggaacactccatcagtgtggatctggatagctccctgtctagtaca 1611
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Qy   2032 tcttccagcagatatgaagattattcagagctgggagagcttcccccacgatctccttta 2091
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Qy   2092 gaaccagtttgtgaagatgggccctttggcccccccaccagaggaaaagaaaaggacatct 2151
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Qy   2152 cgtgagctccgagagctgtggcaaaaggctattcttcaacagatactgc-tgcttagaat 2210
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Qy   2271 gctcgattatgaagaaattactccctgtcttaaagaagtaactacagtgtgggaaaagat 2330
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Qy   2331 gcttagcactccaggaagatcaaaaattaagtttgacatggaaaaaatgcactcggctgt 2390
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Qy   2451 ccaccttaaacaccagtttcccagcaaacagcagccaaaggatgtgccatacaaagaact 2510
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Qy   2571 tacacacccatacttctctgcccagcttggagcaggacagctatcgctttacaacatttt 2630
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Qy   2631 gaaggcctactcacttctagaccaggaagtgggatattgccaaggtctcagctttgtagc 2690
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Qy   2691 aggcattttgcttcttcatatgagtgaggaagaggcgtttaaaatgctcaagtttctgat 2750
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2751 gtttgacatggggctgcggaaacagtatcggccagacatgattattttacagatccagat 2810
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Qy   2931 gttcccgctgggattcgtagccagagtctttgatatgatttttcttcagggaacagaggt 2990
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Qy   2991 catatttaaagtggctttaagtctgttgggaagccataagcccttgattctgcagcatga 3050
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Qy   3051 aaacctagaaaccatagttgactttataaaaagcacgctacccaaccttggcttggtaca 3110
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Db   2523 aaacctagaaaccatagttgactttataaaaagcacgctacccaaccttggcttggtaca 2582

Qy   3111 gatggaaaagaccatcaatcaggtatttgaaatggacatcgctaaacagttacaagctta 3170
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Db   2583 gatggaaaagaccatcaatcaggtatttgaaatggacatcgctaaacagttacaagctta 2642

Qy   3171 tgaagttgagtaccacgtccttcaagaagaacttatcgattcctctcctctcagtgacaa 3230
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Qy   3231 ccaaagaatggataaattagagaaaaccaacagcagcttacgcaaacagaaccttgacct 3290
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Qy   3351 gctcctgagcagtgagagcaagctgaagcaggccatgcttaccttagaactggagcggtc 3410
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Qy   3471 gcctgagtgcacgcagcccgagcccacgggcgactgacagctctgcaggagagattgcaa 3530
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RESULT   5
AAI59640
ID   AAI59640 standard; cDNA; 3281 BP.
XX
AC   AAI59640;
XX
DT   22-OCT-2001  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 3629.
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XX
KW   Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW   peripheral nervous system; neuropathy; central nervous system; CNS;
KW   Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW   amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW   chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW   leukaemia; ss.
XX
OS   Homo sapiens.
XX
PN   WO200153312-A1.
XX
PD   26-JUL-2001.
XX
PF   26-DEC-2000; 2000WO-US34263.
XX
PR   21-JAN-2000; 2000US-0488725.
PR   25-APR-2000; 2000US-0552317.
PR   09-JUL-2000; 2000US-0598042.
PR   19-JUL-2000; 2000US-0620312.
PR   03-AUG-2000; 2000US-0653450.
PR   14-SEP-2000; 2000US-0662191.
PR   19-OCT-2000; 2000US-0693036.
PR   29-NOV-2000; 2000US-0727344.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Asundi V,  Chen R,  Ma Y,  Qian XB,  Ren F,  Wang D;
PI   Wang J,  Wang Z,  Wehrman T,  Xu C,  Xue AJ,  Yang Y,  Zhang J;
PI   Zhao QA,  Zhou P,  Goodrich R,  Drmanac RT;
XX
DR   WPI; 2001-442253/47.
DR   P-PSDB; AAM40484.
XX
PT   Novel nucleic acids and polypeptides, useful for treating disorders
PT   such as central nervous system injuries -
XX
PS   Claim 1; SEQ ID NO 3629; 10078pp; English.
XX
CC   The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC   the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC   immunosuppressant and cytostatic activity. The polynucleotides are useful
CC   in gene therapy. A composition containing a polypeptide or polynucleotide
CC   of the invention may be used to treat diseases of the peripheral nervous
CC   system, such as peripheral nervous injuries, peripheral neuropathy and
CC   localised neuropathies and central nervous system diseases, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC   utilisation of the activities such as: Immune system suppression,
CC   Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC   assays for receptor activity, arthritis and inflammation, leukaemias and
CC   C.N.S disorders.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification.
XX
SQ   Sequence 3281 BP; 912 A; 812 C; 824 G; 733 T; 0 other;


  Query Match             79.7%;  Score 2833.8;  DB 22;  Length 3281;
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  Matches 2983;  Conservative    0;  Mismatches   32;  Indels   20;  Gaps   11;

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Qy    841 cagcccacagatat--cgaggaaaatcgaactat---gctcttcacgattggccagtctg 895
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Qy    896 aagtttacctcatcagtcctgacaccaaaaaaat-----agcattggagaaaaattttaa 950
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Db    361 aagtttacctcatcagtcctgacaccaaaaaaattaggcattgggagaaaaattttaag 420

Qy    951 ggagatatccttttgctctcagggcatcagaca-cgtggaccactttggg-tttatctgt 1008
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Db    421 ggagatatccttttgctctcagggcatcagacaccgtggaccactttggttttatctgt 480

Qy   1009 cgggagtcttccggaggtggcggctttcattttgtctgttacgtgtttcagtgcacaaat 1068
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Qy   1069 gaggctctggttgatgaaattatgatgaccctgaaacaggccttcacggtggccgcagtg 1128
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Qy   1129 cagcagacagctaaggcgccagcccagctgtgtgagggctg--ccccctgcaaagcc--t 1184
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Qy   1185 gcacaagctctgtgagaggatagagggaatgaatt-cttccaaaacaaaactagaactgc 1243
          |||||||||||||||||||||||||||||||||| || ||||||||||||||||||||||
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Qy   1244 aaaagca-cctgacgacattaa-ccaatcaggagcaggcgactatttttgaagaggttca 1301
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Qy   1302 gaaattgagaccgagaaatgagcagcgagagaatgaattgattatttctttttctgagatg 1361
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Db    781 gaaattgagaccgagaaatgagcagcgagagaatgaattgattatttctttttttgagatg 840

Qy   1362 tttatatgaagagaaacagaaagaacacatccatattggggagatgaagcagacatcgca 1421
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Db    841 tttatttgaagagaaacagaaagaacacatccatattggggagatgaagcagacatcgca 900

Qy   1422 gatggcagcagagaatattggaagtgaattaccacccagtgccactcgatttaggctaga 1481
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1482 tatgctgaaaaacaaagcaaagagatctttaacagagtctttagaaagtattttgtcccg 1541
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Qy   1542 gggtaataaagccagaggcctgcaggaacactccatcagtgtggatctggatagctccct 1601
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1602 gtctagtacattaagtaacaccagcaaagagccatctgtgtgtgaaaaggaggccttgcc 1661
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Qy   1662 catctctgagagctcctttaagctcctcggctcctcggaggacctgtccagtgactcgga 1721
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Qy   1722 gagtcatctcccagaagagccagctccgctgtcgccccagcaggccttcaggaggcgagc 1781
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Qy   1782 aaacaccctgagtcacttccccatcgaatgccaggaacctccacaacctgcccgggggtc 1841
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Qy   1842 cccgggggtttcgcaaaggaaacttatgaggtatcactcagtgagcacagagacgcctca 1901
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Qy   1902 tgaacgaaaggactttgaatccaaagcaaaccatcttggtgattctggtgggactcctgt 1961
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Qy   1962 gaagacccggaggcattcctggaggcagcagatattcctccgagtagccaccccgcagaa 2021
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Qy   2022 ggcgtgcgattcttccagcagatatgaagattattcagagctgggagagcttcccccacg 2081
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Qy   2082 atctcctttagaaccagtttgtgaagatgggccctttggccccccaccagaggaaaagaa 2141
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Qy   2142 aaggacatctcgtgagctccgagagctgtggcaaaaggctattcttcaacagatactgct 2201
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Qy   2202 gcttagaatggagaaggaaaatcagaagctccaagcctctgaaaatgatttgctgaacaa 2261
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Qy   2262 gcgcctgaagctcgattatgaagaaattactccctgtcttaaagaagtaactacagtgtg 2321
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Qy   2322 ggaaaagatgcttagcactccaggaagatcaaaaattaagtttgacatggaaaaaatgca 2381
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Qy   2441 ctgagcaattccaccttaaacaccagtttcccagcaaacagcagccaaaggatgtgccat 2500
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Qy   2501 acaaagaactcttaaagcagctgacttcccagcagcatgcgattcttattgaccttgggc 2560
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Qy   2561 gaacctttcctacacacccatacttctctgcccagcttggagcaggacagctatcgcttt 2620
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Qy   2621 acaacattttgaaggcctactcacttctagaccaggaagtgggatattgccaaggtctca 2680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2681 gctttgtagcaggcattttgcttcttcatatgagtgaggaagaggcgtttaaaatgctca 2740
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Qy   2741 agtttctgatgtttgacatggggctgcggaaacagtatcggccagacatgattattttac 2800
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Qy   2801 agatccagatgtaccagctctcgaggttgcttcatgattaccacagagacctctacaatc 2860
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Qy   2861 acctggaggagcacgagatcggccccagcctctacgctgccccctggttcctcaccatgt 2920
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Qy   2921 ttgcctcacagttcccgctgggattcgtagccagagtctttgatatgatttttcttcagg 2980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2981 gaacagaggtcatatttaaagtggctttaagtctgttgggaagccataagcccttgattc 3040
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Qy   3041 tgcagcatgaaaacctagaaaccatagttgactttataaaaagcacgctacccaaccttg 3100
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Qy   3101 gcttggtacagatggaaaagaccatcaatcaggtatttgaaatggacatcgctaaacagt 3160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   3161 tacaagcttatgaagttgagtaccacgtccttcaagaagaacttatcgattcctctcctc 3220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   3221 tcagtgacaaccaaagaatggataaattagagaaaaccaacagcagcttacgcaaacaga 3280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   3281 accttgacctccttgaacagttgcaggtggcaaatggtaggatccaaagccttgaggcca 3340
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Qy   3341 ccattgagaagctcctgagcagtgagagcaagctgaagcaggccatgcttaccttagaac 3400
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Qy   3461 gcgaccgggagcctgagtgcacgcagcccgagcccacgggcgactgacagctctgcagga 3520
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Qy   3521 gagattgcaacaccatcccacactgtccaggcctt 3555
          |||||||||||||||||||||||||||||||||
Db   3001 gagattgcaacaccatcccacactgtccaggcctt 3035
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RESULT 6
AAV05886
ID AAV05886 standard; DNA; 4039 BP.
XX
AC AAV05886;
XX
DT 01-JUN-1998 (first entry)
XX
DE Human Tbc-1 gene.
XX
KW tre-2; BUB2; cdc16; mast cell; probe; hybridisation; subtraction method;
KW mouse; transcription factor; differentiation; proliferation; human; ds;
KW acute myelogenous leukaemia.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 403..3828
FT /*tag= a
FT /product= Tbc1_protein
XX
PN US5700927-A.
XX
PD 23-DEC-1997.

```
XX
PF   23-DEC-1994;   94US-0363300.
XX
PR   23-DEC-1994;   94US-0363300.
XX
PA   (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI   Richardson P,  Zon L;
XX
DR   WPI; 1998-062437/06.
DR   P-PSDB; AAW44777.
XX
PT   DNA encoding Tbc1 polypeptide - useful for treating leukaemia
XX
PS   Claim 3; Fig 1A-B; 22pp; English.
XX
CC   This is the nucleotide sequence which encodes a Tbc1 (tre-2, BUB2 and
CC   cdc16) polypeptide, isolated from a bone marrow-derived mast cell DNA
CC   library.  The screen was carried out using a probe generated by a
CC   subtraction method which compared mRNA expression in an undifferentiated
CC   mast cell line P815 and cell line PGT6 (P815 cells transformed to express
CC   the murine GATA-1 transcription factor - a factor which controls the
CC   expression of genes involved in mast cell differentiation).  Tbc1 encodes
CC   a protein involved in the coupling of cell proliferation to cell
CC   differentiation, which can be used to treat leukaemia (especially acute
CC   myelogenous leukaemia) by causing leukaemic cells to differentiate.
XX
SQ   Sequence 4039 BP; 1042 A; 1096 C; 1060 G; 841 T; 0 other;


  Query Match             70.6%;  Score 2510.4;  DB 19;  Length 4039;
  Best Local Similarity   83.7%;  Pred. No. 0;
  Matches 2949;  Conservative    0;  Mismatches  536;  Indels   37;  Gaps    8;

Qy      1 atggaaccaataacattcacagcaaggaaacatctgctt-cctaacgaggtctcggtgga 59
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Db    292 atggaggcaatcacattcacagcgaggaagcatccgtttccctaacgaagtctccgtgga 351

Qy     60 ttttggcctgcagctggt--gggctccctgcctgtgcattccctgaccaccatgcccatg 117
            || ||| ||||||||||  || ||||| | || |||||||| || ||||| |||||||||
Db    352 cttcggcttgcagctggttgggtctccttacccgtgcattctctcaccactatgcccatg 411

Qy    118 ctgccctgggttgtggctgaggtgcgaagactcagcaggcagtccaccagaaaggaacct 177
          ||||| ||||| || || ||||| ||||||||||  | |||| | | | |||||| |||
Db    412 ctgccgtgggtggtagccgaggtacgaagactcagtggccagtgctctaaaaaggagcct 471

Qy    178 gtaaccaagcaagtccggctttgcgtttcaccctctggactgagatgtgaacctgagcca 237
             || |||||||||| ||||| ||||| |||||| | || || ||||| |
Db    472 aggacaaagcaagtccgcctttgggtttcgccctccggactgcggtgcgagcctgacctg 531

Qy    238 gggagaagtcaacagtgggatcccctgatctattccagcatctttgagtgcaagcctcag 297
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Qy    298 cgtgttcacaaactgattcacaacagtcatgacccaagttactttgcttgtctgattaag 357
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Qy    358 gaagacgctgtccaccggcagagtatctgctatgtgttcaaagccgatgatcaaacaaaa 417
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Qy    418 gtgcctgagatcatcagctccatccgtcaggcggggaagatcgcccggcaggaggagctg 477
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Qy    478 cactgcccgtccgagttcgacgacacgttttccaagaagttcgaggtgctcttctgcggc 537
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Qy    538 cgcgtgacggtggcgcacaagaaggctccgccggccctgatcgacgagtgcatcgagaag 597
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Qy    598 ttcaatcacgtcagcggcagccgggggtccgagagcccccgccccaacccgccccatgcc 657
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Qy    658 gcgcccacagggagccaggagcctgtgcgcaggcccatgcgcaagtccttctcccagccc 717
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Qy    718 ggcctgcgctcgctggcctttaggaaggagctgcaggatgggggcctccgaagcagcggc 777
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Qy    778 ttcttcagctccttcgaggagagcgacattgagaaccacctcattagcggacacaatatt 837
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Qy    838 gtgcagcccacagatatcgaggaaaatcgaactatgctcttcacgattggccagtctgaa 897
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Qy    898 gtttacctcatcagtcctgacaccaaaaaaatagcattggagaaaaattttaaggagata 957
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Qy    958 tccttttgctctcagggcatcagacacgtggaccactttgggtttatctgtcgggagtct 1017
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Qy   1018 tc------cggaggtggcggctttcattttgtctgttacgtgtttcagtgcacaaatgag 1071
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Qy   1072 gctctggttgatgaaattatgatgaccctgaaacaggccttcacggtggccgcagtgcag 1131
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Db   1348 gctctggttgacgagatcatgatgactctgaagcaggctttcacggtagctgcggtgcag 1407

Qy   1132 cagacagctaaggcgccagcccagctgtgtgagggctgccccctgcaaagcctgcacaag 1191
          ||||| |||||||| |||||||||| |||||||||||||||| ||||| ||||||||||
Db   1408 cagacggctaaggcaccagcccagctctgtgagggctgcccctgcaaggcctgcacaag 1467

Qy   1192 ctctgtgagaggatagagggaatgaattcttccaaaacaaaactagaactgcaaaagcac 1251
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Qy   1252 ctgacgacattaaccaatcaggagcaggcgactatttttgaagaggttcagaaattgaga 1311
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Qy   1312 ccgagaaatgagcagcgagagaatgaattgattatttcttttctgagatgtttatatgaa 1371
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Qy   1372 gagaaacagaaagaacacatccatattggggagatgaagcagacatcgcagatggcagca 1431
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Qy   1432 gagaatattggaagtgaattaccacccagtgccactcgatttaggctagatatgctgaaa 1491
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Db   1708 gagaatattgggagtgacctgccacccagtgctagccggttcaggttagattcgctgaag 1767

Qy   1492 aacaaagcaaagagatctttaacagagtctttagaaagtattttgtcccggggtaataaa 1551
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Db   1768 aacagagcaaagaggtccttaacagagtccctagagagcattctgtcccggggtaataaa 1827

Qy   1552 gccagaggcctgcaggaacactccatcagtgtggatctggatagctccctgtctagtaca 1611
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Db   1828 gccagaggcctgcaggaccattccgccagtgtggatctggacagctccacttctagtact 1887

Qy   1612 ttaagtaacaccagcaaagagccatctgtgtgtgaaaaggaggccttgcccatctctgag 1671
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Db   1888 ctaagtaacaccagcaaagagctgtccatgggtgacaaggaggccttccccgtctctgag 1947
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Qy   1672 agctcctttaagctcctcggctcctcggaggacctgtccagtgactcggagagtcatctc 1731
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Qy   1732 ccagaagagccagctccgctgtcgccccagcaggccttcaggaggcgagcaaacaccctg 1791
Db   2008 gcagaagagtctgccctgttgtcaccccagcaggcgttcagaaggagagccaacaccctg 2067

Qy   1792 agtcacttccccatcgaatgccaggaacctccacaacctgcccgggggtccccgggggtt 1851
Db   2068 agtcatttcccagtagagtgccctgcgcctccagaacctgcccagagctctccaggggtc 2127

Qy   1852 tcgcaaaggaaacttatgaggtatcactcagtgagcacagagacgcctcatgaacgaaag 1911
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Qy   1972 aggcattcctggaggcagcagatattcctccgagtagccacccccgcagaaggcgtgcgat 2031
Db   2248 cggcactcgtggagacagcagatattccttcgagtggccactccacagaaggcttgtgac 2307

Qy   2032 tcttccagcagatatgaagattattcagagctgggagagcttcccccacgatctccttta 2091
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Qy   2092 gaaccagtttgtgaagatgggccctttggcccccccaccagaggaaaagaaaaggacatct 2151
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Qy   2152 cgtgagctccgagagctgtggcaaaaggctattcttcaacagatactg-ctgcttagaat 2210
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Qy   2991 catatttaaagtggctttaagtctgttgggaagccataagcccttgattctgcagcatga 3050
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Qy   3231 ccaaagaatggataaattagagaaaaccaacagcagcttacgcaaacagaaccttgacct 3290
Db   3507 ccaaagaatggagaaattggagaaaaccaacagcacgttgcgcaaacagaaccttgacct 3566

Qy   3291 ccttgaacagttgcaggtggcaaatggtaggatccaaagccttgaggccaccattgagaa 3350
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Qy   3351 gctcctgagcagtgagagcaagctgaagcaggccatgcttaccttagaactggagcggtc 3410
Db   3627 acttcttaccagcgagagtaagctgaagcagcgtgcgctgaccctggaggtggagcg--t 3684

Qy   3411 ggccctgctgcagacggtggaggagctgcggcggcggagcgcagagcccagcgaccggga 3470
Db   3685 cgccctgctgcagatggtggaggagctgcggaggcaaagcgcccggcccagcactccaga 3744

Qy   3471 gcctgagtgcacgcagcccgagcccacgggcgactgacagct 3512
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RESULT   7
AAH18401
ID   AAH18401 standard; cDNA; 2362 BP.
XX
AC   AAH18401;
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DT   26-JUN-2001  (first entry)
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DE   Human cDNA sequence SEQ ID NO:18465.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-0116126.
XX
PR   29-JUL-1999;   99JP-0248036.
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PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
PS Claim 8; SEQ ID 18465; 2537pp + CD ROM; English.
XX
CC The present invention describes primer sets for synthesising 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.
XX
SQ Sequence 2362 BP; 657 A; 581 C; 578 G; 546 T; 0 other;

Query Match 59.4%; Score 2112; DB 22; Length 2362;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   1444 agtgaattaccacccagtgccactcgatttaggctagatatgctgaaaaacaaagcaaag 1503
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Db      1 agtgaattaccacccagtgccactcgatttaggctagatatgctgaaaaacaaagcaaag 60

Qy   1504 agatctttaacagagtctttagaaagtattttgtcccggggtaataaagccagaggcctg 1563
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Qy   1564 caggaacactccatcagtgtggatctggatagctccctgtctagtacattaagtaacacc 1623
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Qy   1624 agcaaagagccatctgtgtgtgaaaaggaggccttgcccatctctgagagctccttttaag 1683
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Db    181 agcaaagagccatctgtgtgtgaaaaggaggccttgcccatctctgagagctccttttaag 240

Qy   1684 ctcctcggctcctcggaggacctgtccagtgactcggagagtcatctcccagaagagcca 1743
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Qy   1984 aggcagcagatattcctccgagtagccaccccgcagaaggcgtgcgattcttccagcaga 2043
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Qy   2044 tatgaagattattcagagctgggagagcttcccccacgatctcctttagaaccagtttgt 2103
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Qy   2104 gaagatgggccctttggccccccaccagaggaaaagaaaaggacatctcgtgagctccga 2163
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Qy   2164 gagctgtggcaaaaggctattcttcaacagatactgctgcttagaatggagaaggaaaat 2223
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Db    721 gagctgtggcaaaaggctattcttcaacagatactgctgcttagaatggagaaggaaaat 780

Qy   2224 cagaagctccaagcctctgaaaatgatttgctgaacaagcgcctgaagctcgattatgaa 2283
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Qy   2284 gaaattactccctgtcttaaagaagtaactacagtgtgggaaaagatgcttagcactcca 2343
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Qy   2344 ggaagatcaaaaattaagtttgacatggaaaaaatgcactcggctgttgggcaaggtgtg 2403
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Qy   2404 ccacgtcatcaccgaggtgaaatctggaaatttctagctgagcaattccaccttaaacac 2463
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Qy   2464 cagtttcccagcaaacagcagccaaaggatgtgccatacaaagaactcttaaagcagctg 2523
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Qy   2524 acttcccagcagcatgcgattcttattgaccttgggcgaacctttcctacacacccatac 2583
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Qy   2584 ttctctgcccagcttggagcaggacagctatcgctttacaacattttgaaggcctactca 2643
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Qy   2704 cttcatatgagtgaggaagaggcgtttaaaatgctcaagtttctgatgtttgacatgggg 2763
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Qy    3064 atagttgactttataaaaagcacgctacccaaccttggcttggtacagatggaaaagacc 3123
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Qy    3124 atcaatcaggtatttgaaatggacatcgctaaacagttacaagcttatgaagttgagtac 3183
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Qy    3184 cacgtccttcaagaagaacttatcgattcctctcctctcagtgacaaccaaagaatggat 3243
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Qy    3304 caggtggcaaatggtaggatccaaagccttgaggccaccattgagaagctcctgagcagt 3363
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Qy    3424 acggtggaggagctgcggcggcggagcgcagagcccagcgaccgggagcctgagtgcacg 3483
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Qy    3544 tgtccaggcctt 3555
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RESULT   8
AAS34787
ID   AAS34787 standard; cDNA; 1422 BP.
XX
AC   AAS34787;
XX
DT   04-DEC-2001  (first entry)
XX
DE   cDNA encoding novel human neoplastic disease associated polypeptide #21.
XX
KW   Human; neoplastic disease associated polypeptide; cancer; gene therapy;
KW   hyperproliferative disorder; neural disorder; immune system disorder;
KW   muscular disorder; reproductive disorder; gastrointestinal disorder;
KW   pulmonary disorder; cardiovascular disorder; renal disorder;
KW   neuroprotective; cytostatic; anti inflammatory; vasotropic; ss.
XX
OS   Homo sapiens.
XX
PN   WO200155163-A1.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US01358.
XX
PR   31-JAN-2000; 2000US-0179065.
PR   04-FEB-2000; 2000US-0180628.
PR   24-FEB-2000; 2000US-0184664.
PR   02-MAR-2000; 2000US-0186350.
PR   16-MAR-2000; 2000US-0189874.
PR   17-MAR-2000; 2000US-0190076.
PR   18-APR-2000; 2000US-0198123.
PR   19-MAY-2000; 2000US-0205515.
PR   07-JUN-2000; 2000US-0209467.
PR   28-JUN-2000; 2000US-0214886.
PR   30-JUN-2000; 2000US-0215135.
PR   07-JUL-2000; 2000US-0216647.
PR   07-JUL-2000; 2000US-0216880.
PR   11-JUL-2000; 2000US-0217487.
PR   11-JUL-2000; 2000US-0217496.
PR   14-JUL-2000; 2000US-0218290.
PR   26-JUL-2000; 2000US-0220963.
PR   26-JUL-2000; 2000US-0220964.
PR   14-AUG-2000; 2000US-0224518.
PR   14-AUG-2000; 2000US-0224519.
PR   14-AUG-2000; 2000US-0225213.
PR   14-AUG-2000; 2000US-0225214.
PR   14-AUG-2000; 2000US-0225266.
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PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-465558/50.
DR P-PSDB; AAU21588.
XX
PT Novel polypeptides and polynucleotides useful as diagnostic reagents to
PT diagnose diseases or disorders associated with aberrant expression or
PT activity of polypeptides, and for treating cancers, rheumatoid
PT arthritis -
XX
PS Claim 4; SEQ ID No 31; 687pp; English.
XX
CC The present invention relates to the isolation of novel human neoplastic
CC disease associated polypeptides (AAU21568-AAU21851), and cDNA and DNA
CC sequences encoding for these polypeptides. The sequences of the
CC invention are useful in the diagnosis, treatment, prevention and/or
CC prognosis of disorders involving neoplastic disease such as
CC hyperproliferative disorders (e.g. leukaemia, bone cancer, bladder
CC cancer, brain stem glioma, adult liver cancer, childhood cerebellar
CC astrocytoma, or Hodgkin's lymphoma). The sequences of the invention may
CC also be useful for treating other disorders such as neural disorders,
CC immune system disorders, muscular disorders, reproductive disorders,
CC gastrointestinal disorders, pulmonary disorders, cardiovascular disorders
CC and renal disorders. The polynucleotide sequences of the invention are
CC also useful in gene therapy. AAS34767-AAS35050 represent cDNA sequences
CC encoding for the novel human neoplastic disease associated polypeptides
CC of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1422 BP; 399 A; 322 C; 337 G; 364 T; 0 other;

Query Match 28.2%; Score 1000.8; DB 22; Length 1422;
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Qy   2604 aggacagctatcgctttacaacattttgaaggcctactcacttctagaccaggaagtggg 2663
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XX
DT   06-NOV-2001  (first entry)
XX
DE   Human full-length cDNA, SEQ ID NO: 3914.
XX
KW   Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
XX
OS   Homo sapiens.
XX
PN   EP1130094-A2.
XX
PD   05-SEP-2001.
XX
PF   07-JUL-2000; 2000EP-0114089.
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PR   08-JUL-1999;   99JP-0194486.
PR   11-JAN-2000; 2000JP-0118774.
PR   02-MAY-2000; 2000JP-0183765.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Nishikawa T,  Isogai T,  Hayashi K,  Ishii S,  Kawai Y;
PI   Wakamatsu A,  Sugiyama T,  Nagai K,  Kojima S,  Otsuki T,  Koga H;
XX
DR   WPI; 2001-524255/58.
DR   P-PSDB; AAM93840.
XX
PT   830 Primers useful for synthesizing full length cDNA clones and their
PT   use in genetic manipulation -
XX
PS   Claim 8; SEQ ID NO 3914; 1380pp + sequence listing; English.
XX
CC   The invention relates to primers for synthesising full length cDNA
CC   clones. 830 cDNA molecules encoding a human protein have been
CC   isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC   molecules have been determined. Primers for synthesising the full length
CC   cDNA are useful for clarifying the function of the protein encoded by
CC   the cDNA. The full length clones were obtained by construction of full
CC   length enriched cDNA libraries that were synthesised by the oligo-capping
CC   method. The primers enable the production of the full length cDNA easily
CC   without any special methods. The present sequence is a full length
CC   human cDNA of the invention.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in CD-ROM format directly from EPO.
XX
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RESULT  10
AAS34785
ID   AAS34785 standard; cDNA; 1269 BP.
XX
AC   AAS34785;
XX
DT   04-DEC-2001  (first entry)
XX
DE   cDNA encoding novel human neoplastic disease associated polypeptide #19.
XX
KW   Human; neoplastic disease associated polypeptide; cancer; gene therapy;
KW   hyperproliferative disorder; neural disorder; immune system disorder;
KW   muscular disorder; reproductive disorder; gastrointestinal disorder;
KW   pulmonary disorder; cardiovascular disorder; renal disorder;
KW   neuroprotective; cytostatic; anti inflammatory; vasotropic; ss.
XX
OS   Homo sapiens.
XX
PN   WO200155163-A1.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US01358.
XX
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PR   01-SEP-2000; 2000US-0229343.
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PR   08-SEP-2000; 2000US-0232081.
PR   12-SEP-2000; 2000US-0231968.
PR   14-SEP-2000; 2000US-0232397.
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PR   14-SEP-2000; 2000US-0232401.
PR   14-SEP-2000; 2000US-0233063.
PR   14-SEP-2000; 2000US-0233064.
PR   14-SEP-2000; 2000US-0233065.
PR   21-SEP-2000; 2000US-0234223.
PR   21-SEP-2000; 2000US-0234274.
PR   25-SEP-2000; 2000US-0234997.
PR   25-SEP-2000; 2000US-0234998.
PR   26-SEP-2000; 2000US-0235484.
PR   27-SEP-2000; 2000US-0235834.
PR   27-SEP-2000; 2000US-0235836.
PR   29-SEP-2000; 2000US-0236327.
PR   29-SEP-2000; 2000US-0236367.
PR   29-SEP-2000; 2000US-0236368.
PR   29-SEP-2000; 2000US-0236369.
PR   29-SEP-2000; 2000US-0236370.
PR   02-OCT-2000; 2000US-0236802.
PR   02-OCT-2000; 2000US-0237037.
PR   02-OCT-2000; 2000US-0237038.
PR   02-OCT-2000; 2000US-0237039.
PR   02-OCT-2000; 2000US-0237040.
PR   13-OCT-2000; 2000US-0239935.
PR   13-OCT-2000; 2000US-0239937.
PR   20-OCT-2000; 2000US-0240960.
PR   20-OCT-2000; 2000US-0241221.
PR   20-OCT-2000; 2000US-0241785.
PR   20-OCT-2000; 2000US-0241786.
PR   20-OCT-2000; 2000US-0241787.
PR   20-OCT-2000; 2000US-0241808.
PR   20-OCT-2000; 2000US-0241809.
PR   20-OCT-2000; 2000US-0241826.
PR   01-NOV-2000; 2000US-0244617.
PR   08-NOV-2000; 2000US-0246474.
PR   08-NOV-2000; 2000US-0246475.
PR   08-NOV-2000; 2000US-0246476.
PR   08-NOV-2000; 2000US-0246477.
PR   08-NOV-2000; 2000US-0246478.
PR   08-NOV-2000; 2000US-0246523.
PR   08-NOV-2000; 2000US-0246524.
PR   08-NOV-2000; 2000US-0246525.
PR   08-NOV-2000; 2000US-0246526.
PR   08-NOV-2000; 2000US-0246527.
PR   08-NOV-2000; 2000US-0246528.
PR   08-NOV-2000; 2000US-0246532.
PR   08-NOV-2000; 2000US-0246609.
PR   08-NOV-2000; 2000US-0246610.
PR   08-NOV-2000; 2000US-0246611.
PR   08-NOV-2000; 2000US-0246613.
PR   17-NOV-2000; 2000US-0249207.
PR   17-NOV-2000; 2000US-0249208.
PR   17-NOV-2000; 2000US-0249209.
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PR   17-NOV-2000; 2000US-0249213.
PR   17-NOV-2000; 2000US-0249214.
PR   17-NOV-2000; 2000US-0249215.
PR   17-NOV-2000; 2000US-0249216.
PR   17-NOV-2000; 2000US-0249217.
PR   17-NOV-2000; 2000US-0249218.
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PR   17-NOV-2000; 2000US-0249244.
PR   17-NOV-2000; 2000US-0249245.
PR   17-NOV-2000; 2000US-0249264.
PR   17-NOV-2000; 2000US-0249265.
PR   17-NOV-2000; 2000US-0249297.
PR   17-NOV-2000; 2000US-0249299.
PR   17-NOV-2000; 2000US-0249300.
PR   01-DEC-2000; 2000US-0250160.
PR   01-DEC-2000; 2000US-0250391.
PR   05-DEC-2000; 2000US-0251030.
PR   05-DEC-2000; 2000US-0251988.
PR   05-DEC-2000; 2000US-0256719.
PR   06-DEC-2000; 2000US-0251479.
PR   08-DEC-2000; 2000US-0251856.
PR   08-DEC-2000; 2000US-0251868.
PR   08-DEC-2000; 2000US-0251869.
PR   08-DEC-2000; 2000US-0251989.
PR   08-DEC-2000; 2000US-0251990.
PR   11-DEC-2000; 2000US-0254097.
PR   05-JAN-2001; 2001US-0259678.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Barash SC,  Ruben SM;
XX
DR   WPI; 2001-465558/50.
DR   P-PSDB; AAU21586.
XX
PT   Novel polypeptides and polynucleotides useful as diagnostic reagents to
PT   diagnose diseases or disorders associated with aberrant expression or
PT   activity of polypeptides, and for treating cancers, rheumatoid
PT   arthritis -
XX
PS   Claim 4; SEQ ID No 29; 687pp; English.
XX
CC   The present invention relates to the isolation of novel human neoplastic
CC   disease associated polypeptides (AAU21568-AAU21851), and cDNA and DNA
CC   sequences encoding for these polypeptides. The sequences of the
CC   invention are useful in the diagnosis, treatment, prevention and/or
CC   prognosis of disorders involving neoplastic disease such as
CC   hyperproliferative disorders (e.g. leukaemia, bone cancer, bladder
CC   cancer, brain stem glioma, adult liver cancer, childhood cerebellar
CC   astrocytoma, or Hodgkin's lymphoma). The sequences of the invention may
CC   also be useful for treating other disorders such as neural disorders,
CC   immune system disorders, muscular disorders, reproductive disorders,
CC   gastrointestinal disorders, pulmonary disorders, cardiovascular disorders
CC   and renal disorders. The polynucleotide sequences of the invention are
CC   also useful in gene therapy. AAS34767-AAS35050 represent cDNA sequences
CC   encoding for the novel human neoplastic disease associated polypeptides
CC   of the invention.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1269 BP; 362 A; 313 C; 277 G; 312 T; 5 other;

  Query Match           26.5%;  Score 943.2;  DB 22;  Length 1269;
  Best Local Similarity  98.7%;  Pred. No. 7.7e-247;
  Matches  967;  Conservative    3;  Mismatches    8;  Indels    2;  Gaps    2;

Qy   1908 aaaggactttgaatccaaagcaaaccatcttggtgattctggtgggactcctgtgaagac 1967
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Db    292 aagggactttgaatccaaagcaaaccatcttggtgattctggtgggactcctgtgaagac 351

Qy   1968 ccggaggcattcctggaggcagcagatattcctccgagtagccacccccgcagaaggcgtg 2027
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    352 ccggaggcattcctggaggcagcagatattcctccgagtagccacccccgcagaaggcgtg 411

Qy   2028 cgattcttccagcagatatgaagattattcagagctgggagagcttcccccacgatctcc 2087
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    412 cgattcttccagcagatatgaagattattcagagctgggagagcttcccccacgatctcc 471

Qy   2088 tttagaaccagtttgtgaagatgggccctttggccccccaccagaggaaaagaaaaggac 2147
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    472 tttagaaccagtttgtgaagatgggccctttggccccccaccagaggaaaagaaaaggac 531

Qy   2148 atctcgtgagctccgagagctgtggcaaaaggctattcttcaacagatactgctgcttag 2207
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    532 atctcgtgagctccgagagctgtggcaaaaggctattcttcaacagatactgctgcttag 591

Qy   2208 aatggagaaggaaaatcagaagctccaagcctctgaaaatgatttgctgaacaagcgcct 2267
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    592 aatggagaaggaaaatcagaagctccaagcctctgaaaatgatttgctgaacaagcgcct 651

Qy   2268 gaagctcgattatgaagaaattactccctgtcttaaagaagtaactacagtgtgggaaaa 2327
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Db    652 gaagctcgattatgaagaaattactccctgtcttaaagaagtaactacagtgtgggaaaa 711

Qy   2328 gatgcttagcactccaggaagatcaaaaattaagtttgacatggaaaaaatgcactcggc 2387
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    712 gatgcttagcactccaggaagatcaaaaattaagtttgacatggaaaaaatgcactcggc 771

Qy   2388 tgttgggcaaggtgtgccacgtcatcaccgaggtgaaatctggaaatttctagctgagca 2447
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    772 tgttgggcaaggtgtgccacgtcatcaccgaggtgaaatctggaaatttctagctgagca 831

Qy   2448 attccaccttaaacaccagtttcccagcaaacagcagccaaaggatgtgccatacaaaga 2507
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Db    832 attccaccttaaacaccagtttcccagcaaacagcagccaaaggatgtgccatacaaaga 891

Qy   2508 actcttaaagcagctgacttcccagcagcatgcgattcttattgaccttgggcgaacctt 2567
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Db    892 actcttaaagcagctgacttcccagcagcatgcgattcttattgaccttgggcgaacctt 951

Qy   2568 tcctacacacccatacttctctgcccagcttggagcaggacagctatcgctttacaacat 2627
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Db    952 tcctacacacccatacttctctgcccagcttggagcaggacagctatcgctttacaacat 1011

Qy   2628 tttgaaggcctactcacttctagaccaggaagtgggatattgccaaggtctcagctttgt 2687
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Db   1012 tttgaaggcctactcacttctagaccaggaagtgggatattgccaaggtctcagctttgt 1071

Qy   2688 agcaggcattttgcttcttcatatgagtgaggaagaggcgtttaaaatgctcaagtttct 2747
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1072 agcaggcattttgcttcttcatatgagtgaggaagaggcgtttaaaatgctcaagtttct 1131

Qy   2748 gatgtttgacatggggctgcggaaacagtatcggccagacatgattattttacagatcca 2807
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Db   1132 gatgtttgacatggggctgcggaaacagtatcggccagac-tgattattttacagatcca 1190

Qy   2808 gatgtaccagctctcgaggttgcttcatgattaccacagagacctctacaatcacctgga 2867
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Db   1191 gatgtwccagctytcgargttgcttcatgattaccacagana-ctctaccatcacctgga 1249

Qy   2868 ggagcacgagatcggcccca 2887
           || ||||| ||| | ||||
Db   1250 agaacacgaaatcnggccca 1269


RESULT  11
AAH04450
ID   AAH04450 standard; cDNA; 883 BP.
XX
AC   AAH04450;
XX
DT   26-JUN-2001  (first entry)
XX
DE   Human cDNA clone (5'-primer) SEQ ID NO:1285.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
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PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-0116126.
XX
PR   29-JUL-1999;   99JP-0248036.
PR   27-AUG-1999;   99JP-0300253.
PR   11-JAN-2000; 2000JP-0118776.
PR   02-MAY-2000; 2000JP-0183767.
PR   09-JUN-2000; 2000JP-0241899.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Isogai T,  Nishikawa T,  Hayashi K,  Saito K,  Yamamoto J;
PI   Ishii S,  Sugiyama T,  Wakamatsu A,  Nagai K,  Otsuki T;
XX
DR   WPI; 2001-318749/34.
XX
PT   Primer sets for synthesizing polynucleotides, particularly the 5602
PT   full-length cDNAs defined in the specification, and for the detection
PT   and/or diagnosis of the abnormality of the proteins encoded by the
PT   full-length cDNAs -
XX
PS   Claim 1; SEQ ID 1285; 2537pp + CD ROM; English.
XX
CC   The present invention describes primer sets for synthesising 5602
CC   full-length cDNAs defined in the specification. Where a primer set
CC   comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC   to the complementary strand of a polynucleotide which comprises one of
CC   the 5602 nucleotide sequences defined in the specification, where the
CC   oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC   of an oligonucleotide comprising a sequence complementary to the
CC   complementary strand of a polynucleotide which comprises a 5'-end
CC   sequence and an oligonucleotide comprising a sequence complementary to a
CC   polynucleotide which comprises a 3'-end sequence, where the
CC   oligonucleotide comprises at least 15 nucleotides and the combination of
CC   the 5'-end sequence/3'-end sequence is selected from those defined in
CC   the specification. The primer sets can be used in antisense therapy and
CC   in gene therapy. The primers are useful for synthesising polynucleotides,
CC   particularly full-length cDNAs. The primers are also useful for the
CC   detection and/or diagnosis of the abnormality of the proteins encoded by
CC   the full-length cDNAs. The primers allow obtaining of the full-length
CC   cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC   AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC   AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC   represent oligonucleotides, all of which are used in the exemplification
CC   of the present invention.
XX
SQ   Sequence 883 BP; 245 A; 221 C; 219 G; 193 T; 5 other;


  Query Match             22.1%;  Score 785;  DB 22;  Length 883;
  Best Local Similarity   96.7%;  Pred. No. 9.9e-204;
  Matches  843;  Conservative    0;  Mismatches   23;  Indels    6;  Gaps    4;

Qy   1444 agtgaattaccacccagtgccactcgatttaggctagatatgctgaaaaacaaagcaaag 1503
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Db      1 agtgaattaccacccagtgccactcgatttaggctagatatgctgaaaaacaaagcaaag 60

Qy   1504 agatctttaacagagtctttagaaagtattttgtcccggggtaataaagccagaggcctg 1563
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 agatctttaacagagtctttagaaagtattttgtcccggggtaataaagccagaggcctg 120

Qy   1564 caggaacactccatcagtgtggatctggatagctccctgtctagtacattaagtaacacc 1623
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Db    121 caggaacactccatcagtgtggatctggatagctccctgtctagtacattaagtaacacc 180

Qy   1624 agcaaagagccatctgtgtgtgaaaaggaggccttgcccatctctgagagctcctttaag 1683
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Db    181 agcaaagagccatctgtgtgtgaaaaggaggccttgcccatctctgagagctcctttaag 240

Qy   1684 ctcctcggctcctcggaggacctgtccagtgactcggagagtcatctcccagaagagcca 1743
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Db    241 ctcctcggctcctcggaggacctgtccagtgactcggagagtcatctcccagaagagcca 300

Qy   1744 gctccgctgtcgccccagcaggccttcaggaggcgagcaaacaccctgagtcacttcccc 1803
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Db    301 gctccgctgtcgccccagcaggccttcaggaggcgagcaaacaccctgagtcacttcccc 360

Qy   1804 atcgaatgccaggaacctccacaacctgcccgggggtccccgggggtttcgcaaaggaaa 1863
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Db    361 atcgaatgccaggaacctccacaacctgcccgggggtccccgggggtttcgcaaaggaaa 420

Qy   1864 cttatgaggtatcactcagtgagcacagagacgcctcatgaacgaaaggactttgaatcc 1923
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Db    421 cttatgaggtatcactcagtgagcacagagacgcctcatgaacgaaaggactttgaatcc 480

Qy   1924 aaagcaaaccatcttggtgattctggtgggactcctgtgaagacccggaggcattcctgg 1983
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 aaagcaaaccatcttggtgattctggtgggactcctgtgaagacccggaggcattcctgg 540

Qy   1984 aggcagcagatattcctccgagtagccaccccgcagaaggcgtgcgattcttccagcaga 2043
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 aggcagcagatattcctccgagtagccaccccgcagaaggcgtgcgattcttccagcaga 600

Qy   2044 tatgaagattattcagagctgggagagcttcccccacgatctcctttagaaccagtttgt 2103
            |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    601 tatgaagattattcagagctgggagagctt-ccccacgatctcctttagaaccagtttgt 659

Qy   2104 gaagatgggccctttggccccccaccagaggaaaagaaaaggacatctcgtgagctccga 2163
            |||||||||||||||||||||||||||||||||||||||||||||||||||| ||| |||
Db    660 gaagatgggccctttggccccccaccagaggaaaagaaaaggacatctcgtgagctncga 719

Qy   2164 gagc-tgtggcaaaaggctattcttcaacagatactgctgcttagaatggagaaggaaaa 2222
             ||| ||||||||||||||||||||||||||||||||| |||||| ||||||||||||||
Db    720 aagcttgtggcaaaaggctattcttcaacagatactgntgcttaaaatggagaaggaaaa 779

Qy   2223 tcagaagctccaagcc---tctgaaaatgatttgctgaacaagcgcc-tgaagctcgatt 2278
            ||||||||| | |  |  |   |||  ||||   |||||||||||| ||||  ||||||
Db    780 tcagaagcttccaagccttttgaaaatggattgcttgaacaagcgccttgaacttcgatt 839

Qy   2279 atgaagaaattactccctgtcttaaagaagta 2310
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Db    840 ntgaagaaattactcctggctttaaagaagta 871


RESULT  12
AAK92006
ID   AAK92006 standard; cDNA; 849 BP.
XX
AC   AAK92006;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human cDNA 5'-end sequence, SEQ ID NO: 466.
XX
KW   Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
XX
OS   Homo sapiens.
XX
PN   EP1130094-A2.
XX
PD   05-SEP-2001.
XX
PF   07-JUL-2000; 2000EP-0114089.
XX
PR   08-JUL-1999;   99JP-0194486.
PR   11-JAN-2000; 2000JP-0118774.
PR   02-MAY-2000; 2000JP-0183765.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Nishikawa T,  Isogai T,  Hayashi K,  Ishii S,  Kawai Y;
PI   Wakamatsu A,  Sugiyama T,  Nagai K,  Kojima S,  Otsuki T,  Koga H;
XX
DR   WPI; 2001-524255/58.
XX
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PT 830 Primers useful for synthesizing full length cDNA clones and their
PT use in genetic manipulation -
XX
PS Claim 2; SEQ ID NO 466; 1380pp + sequence listing; English.
XX
CC The invention relates to primers for synthesising full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been
CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC molecules have been determined. Primers for synthesising the full length
CC cDNA are useful for clarifying the function of the protein encoded by
CC the cDNA. The full length clones were obtained by construction of full
CC length enriched cDNA libraries that were synthesised by the oligo-capping
CC method. The primers enable the production of the full length cDNA easily
CC without any special methods. The present sequence is the nucleotide
CC sequence of the 5'-end of a cDNA provided in the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in CD-ROM format directly from EPO.
XX
SQ Sequence 849 BP; 224 A; 195 C; 196 G; 231 T; 3 other;

Query Match 16.2%; Score 574.2; DB 22; Length 849;
Best Local Similarity 98.2%; Pred. No. 3.5e-146;
Matches 642; Conservative 0; Mismatches 6; Indels 6; Gaps 6;

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Db    198 tggggcgaacctttcctacacacccatacttctctgcccagcttggagcaggacagctat 257

Qy   2615 cgctttacaacattttgaaggcctactcacttctagaccaggaagtgggatattgccaag 2674
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    258 cgctttacaacattttgaaggcctactcacttctagaccaggaagtgggatattgccaag 317

Qy   2675 gtctcagctttgtagcaggcattttgcttcttcatatgagtgaggaagaggcgtttaaaa 2734
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    318 gtctcagctttgtagcaggcattttgcttcttcatatgagtgaggaagaggcgtttaaaa 377

Qy   2735 tgctcaagtttctgatgtttgacatggggctgcggaaacagtatcggccagacatgatta 2794
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Db    378 tgctcaagtttctgatgtttgacatggggctgcggaaacagtatcggccagacatgatta 437

Qy   2795 ttttacagatccagatgtaccagctctcgaggttgcttcatgattaccacagagacctct 2854
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Db    438 ttttacagatccagatgtaccagctctcgaggttgcttcatgattaccacagagacctct 497

Qy   2855 acaatcacctggaggagcacgagatcggccccagcctctacgctgccccctggttcctca 2914
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Db    498 acaatcacctggaggagcacgagatcggccccagcctctacgctgccccctggttcctca 557

Qy   2915 ccatgtttgcctcacagttcccgctgggattcgtagccagagtctttgatatgatttttc 2974
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    558 ccatgtttgcctcacagttcccgctgggattcgtagccagagtctttgatatgatttttc 617

Qy   2975 ttcagggaacagaggtcatatttaaagtggctttaagtctgttgggaagccataagccct 3034
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    618 ttcagggaacagaggtcatatttaaagtggctttaagtctgttgggaagccataagccct 677

Qy   3035 tgattctgcagcatgaaaacctagaaaccatagttgactttataaaaagcacgctaccca 3094
          |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db    678 tgattctgcagcatgaaaacctagaaaccatagttgactttataaaaagcacgct-ccca 736

Qy   3095 accttggcttggtacagatggaaaagaccatcaatcaggta-tttgaaatggacatc-gc 3152
          |||||||||||| |||||||||||||||||||||||| ||| |||| |||||||||| |
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Qy   3153 taaacagttacaagcttatg-aagttgagtacca-cgtccttcaagaagaactt 3204
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Db    796 taaacagttacaagcttatgaaagttgagtnccaccgtcctttaagaagaactt 849
```

RESULT 13
AAK93666
ID AAK93666 standard; cDNA; 849 BP.
XX
AC AAK93666;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human cDNA clone representative sequence, SEQ ID NO: 2126.
XX
KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
XX
OS Homo sapiens.
XX
PN EP1130094-A2.
XX
PD 05-SEP-2001.
XX
PF 07-JUL-2000; 2000EP-0114089.
XX
PR 08-JUL-1999; 99JP-0194486.
PR 11-JAN-2000; 2000JP-0118774.
PR 02-MAY-2000; 2000JP-0183765.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
DR WPI; 2001-524255/58.
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their
PT use in genetic manipulation -
XX
PS Example 11; SEQ ID NO 2126; 1380pp + sequence listing; English.
XX
CC The invention relates to primers for synthesising full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been
CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC molecules have been determined. Primers for synthesising the full length
CC cDNA are useful for clarifying the function of the protein encoded by
CC the cDNA. The full length clones were obtained by construction of full
CC length enriched cDNA libraries that were synthesised by the oligo-capping
CC method. The primers enable the production of the full length cDNA easily
CC without any special methods. The present sequence was used as the
CC representative sequence from a human clone which was used in
CC homology searches to identify the clone.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in CD-ROM format directly from EPO.
XX
SQ Sequence 849 BP; 224 A; 195 C; 196 G; 231 T; 3 other;

Query Match 16.2%; Score 574.2; DB 22; Length 849;
Best Local Similarity 98.2%; Pred. No. 3.5e-146;
Matches 642; Conservative 0; Mismatches 6; Indels 6; Gaps 6;

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Qy   2555 ttgggcgaacctttcctacacacccatacttctctgcccagcttggagcaggacagctat 2614
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Qy   2615 cgctttacaacattttgaaggcctactcacttctagaccaggaagtgggatattgccaag 2674
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Qy   2675 gtctcagctttgtagcaggcattttgcttcttcatatgagtgaggaagaggcgtttaaaa 2734
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Qy   2735 tgctcaagtttctgatgtttgacatggggctgcggaaacagtatcggccagacatgatta 2794
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Qy   2795 ttttacagatccagatgtaccagctctcgaggttgcttcatgattaccacagagacctct 2854
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```

```
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Qy   2915 ccatgtttgcctcacagttcccgctgggattcgtagccagagtctttgatatgatttttc 2974
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    558 ccatgtttgcctcacagttcccgctgggattcgtagccagagtctttgatatgatttttc 617

Qy   2975 ttcagggaacagaggtcatatttaaagtggctttaagtctgttgggaagccataagccct 3034
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    618 ttcagggaacagaggtcatatttaaagtggctttaagtctgttgggaagccataagccct 677

Qy   3035 tgattctgcagcatgaaaacctagaaaccatagttgactttataaaaagcacgctaccca 3094
          |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db    678 tgattctgcagcatgaaaacctagaaaccatagttgactttataaaaagcacgct-ccca 736

Qy   3095 accttggcttggtacagatggaaaagaccatcaatcaggta-tttgaaatggacatc-gc 3152
          |||||||||||| |||||||||||||||||||| ||| |||| |||||||||| |
Db    737 accttggcttgg-acagatggaaaagaccatcaatcangtattttgnaatggacatcggt 795

Qy   3153 taaacagttacaagcttatg-aagttgagtacca-cgtccttcaagaagaactt 3204
          |||||||||||||||||| ||||||||| ||| ||||||| ||||||||||
Db    796 taaacagttacaagcttatgaaagttgagtnccaccgtcctttaagaagaactt 849
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RESULT 14
AAZ50904
ID AAZ50904 standard; DNA; 17590 BP.
XX
AC AAZ50904;
XX
DT 31-MAY-2000 (first entry)
XX
DE Human TBC-1 partial genomic DNA comprising 5' end sequence.
XX
KW TBC-1; human; biallelic marker; chromosome 4; cell cycle regulator; SNP;
KW Single nucleotide polymorphism; tissue differentiation; prostate cancer;
KW linkage analysis; genetic map; detection; diagnosis; genotyping;
KW transgenic animal; screening; ds.
XX
OS Homo sapiens.
XX

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FT		/*tag= a
FT		/note= "5' Regulatory region"
FT	exon	2001..2077
FT		/*tag= b
FT		/number= 1
FT	intron	2078..12739
FT		/*tag= c
FT		/number= 1
FT	misc_feature	9391..9845
FT		/*tag= d
FT		/note= "Amplicon 99-430"
FT	primer_bind	9391..9408
FT		/*tag= e
FT		/bound_moiety= "Primer B1"
FT		/note= "Amplification of amplicon 99-430"
FT	primer_bind	9475..9493
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FT		/bound_moiety= "Primer D1"
FT		/note= "Microsequencing of marker 99-430-352"
FT	misc_binding	9482..9506
FT		/*tag= g
FT		/bound_moiety= "Probe P1"
FT		/note= "Detection of Biallelic marker 99-430-352"
FT	misc_feature	9494
FT		/*tag= h
FT		/note= "Ambiguity base 'R' corresponds to 'A' in allele-1
FT		and 'G' in allele-2 of biallelic marker 99-430-352"
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FT		/bound_moiety= "Primer C1"
FT		/note= "Amplification of amplicon 99-430"
FT	exon	12292..12373
FT		/*tag= k
FT		/number= 1 bis
FT	intron	12374..12739
FT		/*tag= l
FT		/number= 1 bis
FT	exon	12740..13249
FT		/*tag= m
FT		/number= 2
FT	intron	13250..17590
FT		/*tag= n
FT		/number= 2

XX
PN WO200008209-A2.
XX
PD 17-FEB-2000.
XX
PF 06-AUG-1999; 99WO-IB01444.
XX
PR 07-AUG-1998; 98US-0095653.
XX
PA (GEST) GENSET.
XX
PI Blumenfeld M, Bougueleret L, Chumakov I;
XX
DR WPI; 2000-205736/18.
XX
PT New isolated human TBC-1 nucleic acids, useful for developing products
PT for the diagnosis and treatment of disorders involving cell
PT proliferation, particularly prostate cancer
XX
PS Claim 1; Page 93-100; 166pp; English.
XX
CC The present sequence is the partial genomic DNA of human TBC-1 gene,
CC comprising the 5' regulatory region, exons 1, 1bis and 2. TBC-1 gene is
CC mapped to a candidate region of prostate cancer on chromosome 4. Single
CC nucleotide polymorphism (SNP) is located within the biallelic marker
CC region 99-430-352, localised in intron 1 of TBC-1 genomic DNA.
CC TBC-1 gene is involved in the regulation of cell cycle and tissue
CC differentiation in mammals. An alteration of TBC-1 sequence may be
CC associated with a pathological condition, resulting in abnormal cell
CC proliferation leading to cancer, e.g. prostate cancer. The biallelic
CC markers can be used for generation of genetic maps, linkage analysis and
CC association studies. TBC-1 sequence can be used for detection,
CC diagnosis, genotyping, production of transgenic animals and screening
CC of compounds for use in therapy.
XX
SQ Sequence 17590 BP; 4760 A; 3776 C; 4104 G; 4919 T; 31 other;

Query Match 11.9%; Score 422.6; DB 21; Length 17590;
Best Local Similarity 95.8%; Pred. No. 5.4e-104;
Matches 434; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

```
Qy      1 atggaaccaataacattcacagcaaggaaacatctgcttcctaacgaggtctcggtggat 60
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Db  12833 atggaaccaataacattcacagcaaggaaacatctgctttctaacgaggtctcggtggat 12892

Qy     61 tttggcctgcagctggtgggctccctgcctgtgcattccctgaccaccatgcccatgctg 120
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Db  12893 tttggcctgcagctggtgggctccctgcctgtgcattccctgaccaccatgcccatgctg 12952

Qy    121 ccctgggttgtggctgaggtgcgaagactcagcaggcagtccaccagaaaggaacctgta 180
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Qy     181 accaagcaagtccggctttgcgtttcaccctctggactgagatgtgaacctgagccaggg 240
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Db   13013 accaagcaagtccggctttgcgtttcaccctctggactgagatgtgaacctgagccaggg 13072

Qy     241 agaagtcaacagtgggatcccctgatctattccagcatctttgagtgcaagcctcagcgt 300
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Db   13073 agaagtcaacagtgggatcccctgatctattccagcatctttgagtgcaagcctcagcgt 13132

Qy     301 gttcacaaactgattcacaacagtcatgacccaagttactttgcttgtctgattaaggaa 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   13133 gttcacaaactgattcacaacagtcatgacccaagttactttgcttgtctgattaaggaa 13192

Qy     361 gacgctgtccaccggcagagtatctgctatgtgttcaaagccgatgatcaaacaaaagtg 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   13193 gacgctgtccaccggcagagtatctgctatgtgttcaaagccgatgatcaaacaaaagta 13252

Qy     421 cctgagatcatcagctccatccgtcaggcgggg 453
             ||||||    | |   |   | ||| | ||
Db   13253 agtgagatggagatccaaaagactaaggtgtgg 13285
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RESULT 15
AAZ15229
ID AAZ15229 standard; cDNA; 696 BP.
XX
AC AAZ15229;
XX
DT 12-OCT-1999 (first entry)
XX
DE Human gene expression product cDNA sequence SEQ ID NO:2698.
XX
KW Human; gene; gene expression product; diagnosis; therapy; probe;
KW detection; mapping; tissue typing; profiling; forensic; cancer;
KW genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
XX
OS Homo sapiens.
XX
PN WO9938972-A2.
XX
PD 05-AUG-1999.
XX
PF 28-JAN-1999; 99WO-US01619.
XX
PR 03-APR-1998; 98US-0080666.
PR 28-JAN-1998; 98US-0072910.
PR 24-FEB-1998; 98US-0075954.
PR 31-MAR-1998; 98US-0080114.
PR 03-APR-1998; 98US-0080515.
XX
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
XX
PI Crkvenjakov R, Dickson M, Drmanac R, Drmanac S;
PI Escobedo J, Garcia PD, Garcia V, Giese K, Innis MA;
PI Jones WL, Kassam A, Kennedy GC, Kita D, Labat I;
PI Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard C;
PI Stache-Crain B, Sudduth-Klinger J, Williams LT;
XX
DR WPI; 1999-494092/41.
XX
PT Novel human genes and their expression products which are
PT differentially expressed in different cell types
XX
PS Claim 1; Page 1311; 2479pp; English.
XX
CC The present invention describes a library of human polynucleotides
CC comprising the sequences given in AAZ12532 to AAZ17779. Also described is
CC a method of detecting differentially expressed genes correlated with the
CC cancerous state of a mammalian cell, comprising detecting at least one
CC differentially expressed gene product in a test sample from a cell
CC suspected of being cancerous, where the gene product is encoded by one
CC of the 5248 polynucleotide sequences given in AAZ12532 to AAZ17779. The
CC polynucleotides can be used as a source of primers and probes, which can
CC be used for a variety of purpose, e.g. detection of expression levels,
CC mapping, tissue typing or profiling, forensics, genetic analysis and
CC detection of polymorphisms. Polypeptides encoded by the polynucleotides
CC can be used for raising antibodies for experimental, diagnostic and
CC therapeutic purposes. The polynucleotides may also be used to construct
CC arrays for diagnostics (which may be used to determine function of an
CC encoded protein); and to detect differences in expression levels between
CC two cells (e.g. to identify abnormal or diseased tissue in a human, to
CC identify a genetic predisposition or susceptibility to a disease such as
CC cancer). The polynucleotides of the invention are especially used in the
CC diagnosis, prognosis and management of colorectal cancer, breast cancer,
CC and lung cancer. The polynucleotides can also be used to screen for
CC peptide analogues and antagonists.
XX
SQ Sequence 696 BP; 189 A; 157 C; 178 G; 142 T; 30 other;

Query Match 10.2%; Score 362; DB 20; Length 696;
Best Local Similarity 100.0%; Pred. No. 2.8e-88;
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    3194 aagaagaacttatcgattcctctcctctcagtgacaaccaaagaatggataaattagaga 3253
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Db      59 aagaagaacttatcgattcctctcctctcagtgacaaccaaagaatggataaattagaga 118

Qy    3254 aaaccaacagcagcttacgcaaacagaaccttgacctccttgaacagttgcaggtggcaa 3313
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     119 aaaccaacagcagcttacgcaaacagaaccttgacctccttgaacagttgcaggtggcaa 178

Qy    3314 atggtaggatccaaagccttgaggccaccattgagaagctcctgagcagtgagagcaagc 3373
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Db     179 atggtaggatccaaagccttgaggccaccattgagaagctcctgagcagtgagagcaagc 238

Qy    3374 tgaagcaggccatgcttaccttagaactggagcggtcggccctgctgcagacggtggagg 3433
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Db     239 tgaagcaggccatgcttaccttagaactggagcggtcggccctgctgcagacggtggagg 298

Qy    3434 agctgcggcggcggagcgcagagcccagcgaccgggagcctgagtgcacgcagcccgagc 3493
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Qy    3494 ccacgggcgactgacagctctgcaggagagattgcaacaccatcccacactgtccaggcc 3553
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     419 tt 420
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Search completed: September 9, 2002, 19:20:22
Job time: 17600 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: September 9, 2002, 19:16:17 ; Search time 8477.27 Seconds
(without alignments)
8775.683 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
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11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	2510.4	70.6	4039	6	I86429	I86429 Sequence 1
3	2510.4	70.6	4039	10	MMU33005	U33005 Mus musculu
4	2340	65.8	2576	9	AB029031	AB029031 Homo sapi
5	2112	59.4	2362	9	AK027355	AK027355 Homo sapi
6	1359.2	38.2	1995	4	BTA17923	Y17923 Bos taurus
7	1179.6	33.2	3051	10	BC004675	BC004675 Mus muscu
8	998.4	28.1	1788	9	AK057182	AK057182 Homo sapi
9	682.2	19.2	5922	9	AB011175	AB011175 Homo sapi
c 10	465.8	13.1	189811	30	AC009595	Ac009595 Homo sapi
11	465.8	13.1	195108	9	AC021106	AC021106 Homo sapi
c 12	465.8	13.1	208318	2	AC108933	AC108933 Homo sapi
c 13	424.2	11.9	110000	2	AL390202_04	Continuation (5 of
14	304.6	8.6	3214	3	DMU50542	U50542 Drosophila
15	304.6	8.6	4746	3	DME17919	Y17919 Drosophila
16	284.4	8.0	189811	30	AC009595	Ac009595 Homo sapi
17	284.4	8.0	208318	2	AC108933	AC108933 Homo sapi
18	252.4	7.1	163928	2	AC021335	AC021335 Homo sapi
19	252.4	7.1	180918	9	AC098680	AC098680 Homo sapi
20	245.6	6.9	17019	2	AC019886	AC019886 Drosophil
21	245.6	6.9	161117	3	AC008311	AC008311 Drosophil
22	245.6	6.9	168448	3	AC009346	AC009346 Drosophil
23	245.6	6.9	297832	3	AE003602	AE003602 Drosophil
c 24	180	5.1	163928	2	AC021335	AC021335 Homo sapi
25	141.8	4.0	3761	9	BC014111	BC014111 Homo sapi
c 26	141	4.0	221717	2	AC074357	AC074357 Mus muscu
c 27	139.2	3.9	158310	9	AL162571	AL162571 Human DNA
28	139.2	3.9	183577	2	AC011164	AC011164 Homo sapi
29	132.8	3.7	3691	6	AX078376	AX078376 Sequence
30	132.8	3.7	4560	9	HSA011679	AJ011679 Homo sapi
31	123.8	3.5	154	6	AX261661	AX261661 Sequence
32	119.4	3.4	14119	2	AC013898	AC013898 Drosophil
c 33	119.4	3.4	164413	3	AC023718	AC023718 Drosophil
c 34	119.4	3.4	303648	3	AE003486	AE003486 Drosophil
35	114.6	3.2	2013	9	AF042345	AF042345 Homo sapi
36	114.6	3.2	7383	9	AF008915	AF008915 Homo sapi
c 37	101.8	2.9	30027	3	CELT24D11	U49940 Caenorhabdi
c 38	98	2.8	20553	3	CBRG26M15	AC084540 Caenorhab
c 39	95.6	2.7	73803	8	NCB11B22	AL356834 Neurospor
40	90	2.5	5870	10	MMU53586	U53586 Mus musculu
c 41	84.2	2.4	441	11	G47994	G47994 Z27058_1 Ze
42	80	2.3	27102	3	U41540	U41540 Caenorhabdi
c 43	79.6	2.2	110032	2	AC014916	AC014916 Drosophil
44	79.6	2.2	159660	3	AC010040	AC010040 Drosophil
45	79.6	2.2	282267	3	AE003555	AE003555 Drosophil

ALIGNMENTS

RESULT 1
BC014529
LOCUS BC014529 3023 bp mRNA linear PRI 19-DEC-2001
DEFINITION Homo sapiens, clone IMAGE:3843156, mRNA.
ACCESSION BC014529
VERSION BC014529.1 GI:17939551
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3023)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (24-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 14 Row: c Column: 16
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

FEATURES Location/Qualifiers
source 1. .3023
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/db_xref="taxon:9606"
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BASE COUNT 883 a 712 c 740 g 688 t
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Query Match 77.4%; Score 2751; DB 9; Length 3023;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2751; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    805 attgagaaccacctcattagcggacacaatattgtgcagcccacagatatcgaggaaaat 864
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Db     10 ATTGAGAACCACCTCATTAGCGGACACAATATTGTGCAGCCCACAGATATCGAGGAAAAT 69

Qy    865 cgaactatgctcttcacgattggccagtctgaagtttacctcatcagtcctgacaccaaa 924
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Db     70 CGAACTATGCTCTTCACGATTGGCCAGTCTGAAGTTTACCTCATCAGTCCTGACACCAAA 129

Qy    925 aaaatagcattggagaaaaatttttaaggagatatccttttgctctcagggcatcagacac 984
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RESULT   2
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LOCUS       I86429                 4039 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 1 from patent US 5700927.
ACCESSION   I86429
VERSION     I86429.1  GI:3206147
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4039)
  AUTHORS   Zon,L. and Richardson,P.
  TITLE     Tbc1 gene and uses thereof
  JOURNAL   Patent: US 5700927-A 1 23-DEC-1997;
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BASE COUNT     1042 a   1096 c   1060 g    841 t
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RESULT   3
MMU33005
LOCUS       MMU33005                4039 bp    mRNA    linear   ROD 12-JAN-1996
DEFINITION  Mus musculus tbc1 mRNA, complete cds.
ACCESSION   U33005
VERSION     U33005.1  GI:988220
KEYWORDS    .
SOURCE      house mouse.
  ORGANISM  Mus musculus
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REFERENCE   1  (bases 1 to 4039)
  AUTHORS   Richardson,P.M. and Zon,L.I.
  TITLE     Molecular cloning of a cDNA with a novel domain present in the
            tre-2 oncogene and the yeast cell cycle regulators BUB2 and cdc16
  JOURNAL   Oncogene 11 (6), 1139-1148 (1995)
  MEDLINE   96032578
   PUBMED   7566974
REFERENCE   2  (bases 1 to 4039)
  AUTHORS   Richardson,P.M. and Zon,L.I.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-1995) Leonard I. Zon, Hematology, Childrens
            Hospital of Boston, HHMI, 300 Longwood Ave., Boston, MA 02115, USA
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ORIGIN


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Qy     238 gggagaagtcaacagtgggatcccctgatctattccagcatctttgagtgcaagcctcag 297
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Qy     298 cgtgttcacaaactgattcacaacagtcatgacccaagttactttgcttgtctgattaag 357
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Qy     418 gtgcctgagatcatcagctccatccgtcaggcggggaagatcgcccggcaggaggagctg 477
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Qy     478 cactgcccgtccgagttcgacgacacgttttccaagaagttcgaggtgctcttctgcggc 537
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Qy     538 cgcgtgacggtggcgcacaagaaggctccgccggccctgatcgacgagtgcatcgagaag 597
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Qy     598 ttcaatcacgtcagcggcagccgggggtccgagagcccccgccccaacccgccccatgcc 657
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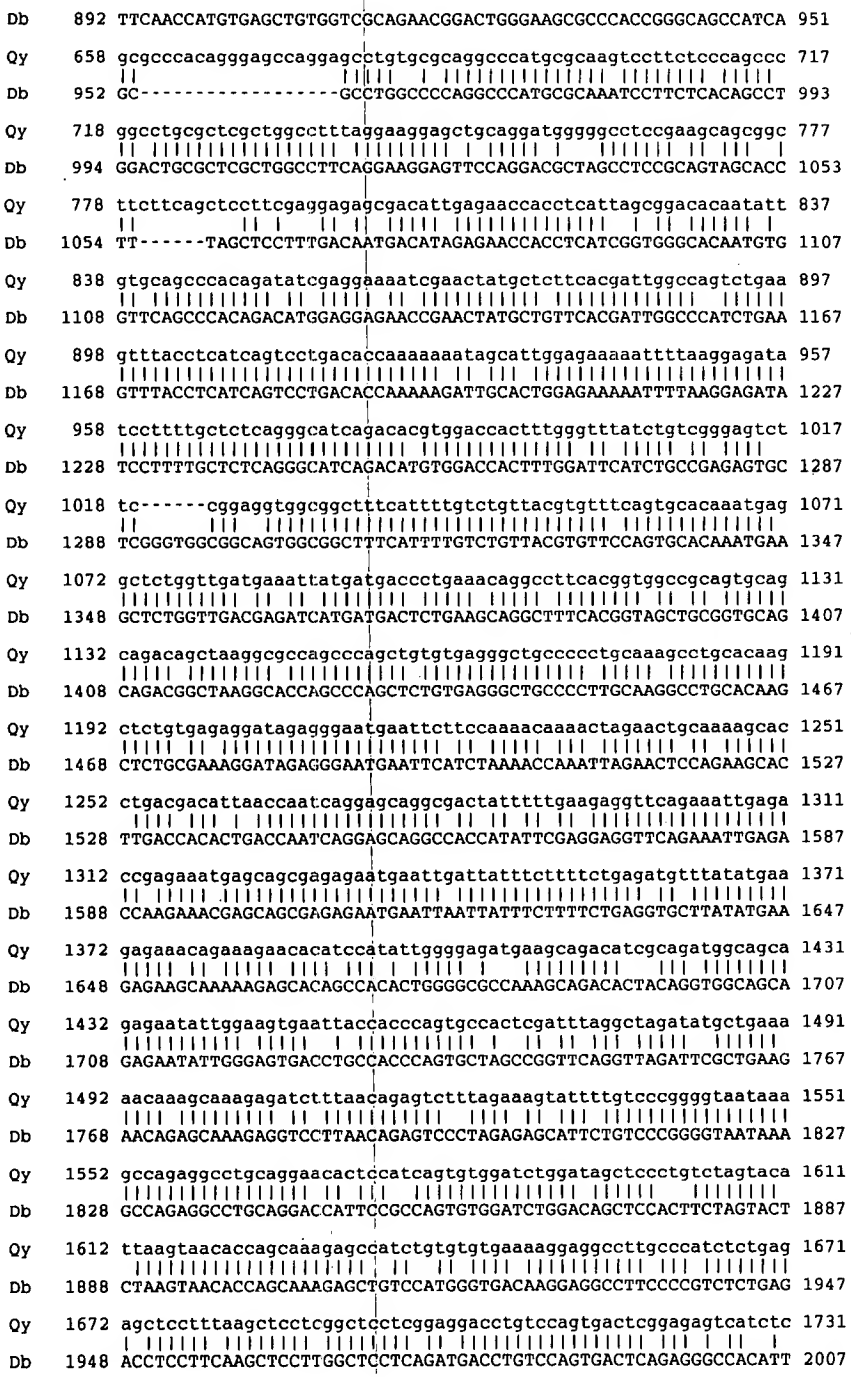
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Db   3087 GTACCAGCTGTCACGGCTCCTCCACGATTACCACCGAGACCTCTACAACCACCTGGAAGA 3146

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Qy   2931 gttcccgctgggattcgtagccagagtctttgatatgatttttcttcagggaacagaggt 2990
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Qy   2991 catatttaaagtggctttaagtctgttgggaagccataagcccttgattctgcagcatga 3050
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Db   3267 CATATTTAAAGTAGCTTTAAGTCTTTTGGGGAGCCATAAGCCCTTGATTCTACAGCATGA 3326

Qy   3051 aaacctagaaaccatagttgactttataaaaagcacgctacccaaccttggcttggtaca 3110
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Db   3327 GAACCTGGAAACCATCGTGGACTTCATAAAGAACACACTCCCCAACCTGGGCCTGGTGCA 3386

Qy   3111 gatggaaaagaccatcaatcaggtatttgaaatggacatcgctaaacagttacaagctta 3170
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Qy   3171 tgaagttgagtaccacgtccttcaagaagaacttatcgattcctctcctctcagtgacaa 3230
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Qy   3231 ccaaagaatggataaattagagaaaaccaacagcagcttacgcaaacagaaccttgacct 3290
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Qy   3291 ccttgaacagttgcaggtggcaaatggtaggatccaaagccttgaggccaccattgagaa 3350
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Qy   3351 gctcctgagcagtgagagcaagctgaagcaggccatgcttaccttagaactggagcggtc 3410
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Db   3627 ACTTCTTACCAGCGAGAGTAAGCTGAAGCAGCGTGCGCTGACCCTGGAGGTGGAGCG--T 3684

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VERSION     AB029031.1  GI:5689552
KEYWORDS    .
SOURCE      Homo sapiens brain cDNA to mRNA, clone_lib:pBluescriptII SK plus
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REFERENCE   1  (sites)
  AUTHORS   Kikuno,R., Nagase,T., Ishikawa,K., Hirosawa,M., Miyajima,N.,
            Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.
  TITLE     Prediction of the coding sequences of unidentified human genes.
            XIV. The complete sequences of 100 new cDNA clones from brain which
            code for large proteins in vitro
  JOURNAL   DNA Res. 6 (3), 197-205 (1999)
  MEDLINE   99397452
REFERENCE   2  (bases 1 to 2576)
  AUTHORS   Ohara,O., Nagase,T. and Kikuno,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JUN-1999) Osamu Ohara, Kazusa DNA Research Institute,
            Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba
            292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913,
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ORIGIN
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Qy   1276 caggcgactatttttgaagaggttcagaaattgagaccgagaaatgagcagcgagagaat 1335
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Qy   1576 atcagtgtggatctggatagctccctgtctagtacattaagtaacaccagcaaagagcca 1635
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DEFINITION  Homo sapiens cDNA FLJ14449 fis, clone HEMBB1001684.
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VERSION     AK027355.1  GI:14041975
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens embryo, 10 weeks whole embryo, mainly body cDNA to
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REFERENCE   1  (sites)
  AUTHORS   Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
            Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H.,
            Wagatsuma,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H.,
            Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K.,
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            Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2362)
  AUTHORS   Isogai,T. and Otsuki,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,
            Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology; cDNA library construction,
            5'- & 3'-end one pass sequencing and clone selection: Helix
            Research Institute (supported by Japan Key Technology Center etc.)
            and Department of Virology, Institute of Medical Science,
            University of Tokyo
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BASE COUNT      657 a    581 c    578 g    546 t
ORIGIN


  Query Match           59.4%;  Score 2112;  DB 9;  Length 2362;
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Db   1921 GAGAGCAAGCTGAAGCAGGCCATGCTTACCTTAGAACTGGAGCGGTCGGCCCTGCTGCAG 1980

Qy   3424 acggtggaggagctgcggcggcggagcgcagagcccagcgaccgggagcctgagtgcacg 3483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 ACGGTGGAGGAGCTGCGGCGGCGGAGCGCAGAGCCCAGCGACCGGGAGCCTGAGTGCACG 2040

Qy   3484 cagcccgagcccacgggcgactgacagctctgcaggagagattgcaacaccatcccacac 3543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 CAGCCCGAGCCCACGGGCGACTGACAGCTCTGCAGGAGAGATTGCAACACCATCCCACAC 2100

Qy   3544 tgtccaggcctt 3555
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Db   2101 TGTCCAGGCCTT 2112
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RESULT   6
BTA17923
LOCUS       BTA17923                1995 bp    mRNA    linear   MAM 18-NOV-1998
DEFINITION  Bos taurus mRNA for lyncein.
ACCESSION   Y17923
VERSION     Y17923.1  GI:3893076
KEYWORDS    lyn gene; lyncein.
SOURCE      cow.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 1995)
  AUTHORS   Xu,X.Z., Wes,P.D., Chen,H., Li,H.S., Yu,M., Morgan,S., Liu,Y. and
            Montell,C.
  TITLE     Retinal targets for calmodulin include proteins implicated in
            synaptic transmission
  JOURNAL   J. Biol. Chem. 273 (47), 31297-31307 (1998)
  MEDLINE   99030403
REFERENCE   2  (bases 1 to 1995)
  AUTHORS   Montell,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-AUG-1998) C. Montell, The Johns Hopkins University
            School of Medicine, Department of Biological Chermistry, 725 N.
            Wolfe Street, Baltimore, MD 21205-2185, USA
FEATURES             Location/Qualifiers
     source          1. .1995
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
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                     VLQEELIDSSPLSDNQRMDKLEKTNSSLRKQNLDLLEQLQVANGRIQSLEATVEKLLT
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BASE COUNT      560 a    516 c    497 g    422 t
ORIGIN
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Db      9 CAGGGGTCTCGCAAAGGAAACTTGTGAGGTATCACTCAGTGAGCACAGAGACGCCTCATG 68

Qy   1904 aacgaaaggactttgaatccaaagcaaaccatcttggtgattctggtgggactcctgtga 1963
          ||||||||||||||| ||||||||  ||||  |  | ||| |  |  |||| |||||||
Db     69 AACGAAAGGACTTTGAGTCCAAAGCCGACCACATCAGCGATGCCAGCAGGACCCCTGTGA 128

Qy   1964 agacccggaggcattcctggaggcagcagatattcctccgagtagccaccccgcagaaagg 2023
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Qy   2084 ctcctttagaaccagtttgtgaagatgggccctttggccccccaccagaggaaaagaaaa 2143
          ||||  |||||||||||||||||||| ||||||||||    ||||||||||||||||||
Db    249 CTCCACTAGAACCAGTTTGTGAAGATGGACCCTTTGGCCCGGTCCCAGAGGAAAAGAAAA 308

Qy   2144 ggacatctcgtgagctccgagagctgtggcaaaaggctattcttcaacagatactgctgc 2203
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Db    309 GAACATCTCATGAACTTCGGGAGCTGTGGCAAAAGGCCATTCTACAACAGATATTGCTGC 368

Qy   2204 ttagaatggagaaggaaaatcagaagctccaagcctctgaaaatgatttgctgaacaagc 2263
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Db    369 TCAGGATGGAGAAAGAAAACCAAAAACTGCAAGCCTCTGAGAATGATTTGCTGAACAAGC 428

Qy   2264 gcctgaagctcgattatgaagaaattactccctgtcttaaagaagtaactacagtgtggg 2323
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Db    429 GCCTAAAGCTTGATTATGAAGAAATCACTCCCTGTCTTAAAGAAGTGACTACAGTGTGGG 488

Qy   2324 aaaagatgcttagcactccaggaagatcaaaaattaagtttgacatggaaaaaatgcact 2383
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Db    489 AAAAGATACTTAGCACTCCAGGAAGATCAAAAATTAAGTTTGACATGGAAAAAATGCACT 548

Qy   2384 cggctgttgggcaaggtgtgccacgtcatcaccgaggtgaaatctggaaatttctagctg 2443
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Qy   2444 agcaattccaccttaaacaccagtttcccagcaaacagcagccaaaggatgtgccataca 2503
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Db    609 AGCAGTACCACCTGAAGCACCCGTTTCCCTGCAAACAGCAGCCCAAGGACACGCCCTACA 668

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Qy   2744 ttctgatgtttgacatggggctgcggaaacagtatcggccagacatgattattttacaga 2803
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Qy   2804 tccagatgtaccagctctcgaggttgcttcatgattaccacagagacctctacaatcacc 2863
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Qy   2864 tggaggagcacgagatcggccccagcctctacgctgccccctggttcctcaccatgtttg 2923
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Qy   2984 cagaggtcatatttaaagtggctttaagtctgttgggaagccataagcccttgattctgc 3043
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Qy   3044 agcatgaaaacctagaaaccatagttgactttataaaaagcacgctacccaaccttggct 3103
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Db   1269 TGGTGCAGATGGAGAAGACTATCAGTCAGGTGTTTGAGACGGACATCTCGAAACAGTTAC 1328

Qy   3164 aagcttatgaagttgagtaccacgtccttcaagaagaacttatcgattcctctcctctca 3223
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RESULT   7
BC004675
LOCUS       BC004675               3051 bp    mRNA    linear   ROD 19-JUL-2001
DEFINITION  Mus musculus, clone IMAGE:3500261, mRNA, partial cds.
ACCESSION   BC004675
VERSION     BC004675.1  GI:14919386
KEYWORDS    .
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 3051)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-MAR-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey Green M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: villalon@bcm.tmc.edu.
            Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
            A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
            Muzny,D.M., Gibbs,R.A.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 9 Row: m Column: 4.
FEATURES             Location/Qualifiers
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ORIGIN
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Db      1 GCTTGTGACTCCCCGAGCAGATATGAAGATTATTCCGAGCTGGGAGAGCTCCCTCCACGC 60

Qy   2083 tctcctttagaaccagtttgtgaagatgggccctttggccccccaccagaggaaaagaaa 2142
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Db     121 AAGACGTCACGCGAGCTTCGAGAGCTGTGGAAAAAGGCCATCTTGCAGCAGATCCTGCTG 180

Qy    2203 cttagaatggagaaggaaaatcagaagctccaagcctctgaaaatgatttgctgaacaag 2262

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Db     301 GAAAAGATGCTTAGCACTCCAGGAAGATCCAAAATTAAGTTTGACATGGAAAAAGTGCAC 360

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Db     361 TCAGCTGTTGGGCAAGGTGTGCCACGTCATCACCGAGGTGAGATCTGGAAATTTCTAGCT 420

Qy    2443 gagcaattccaccttaaacaccagtttcccagcaaacagcagccaaaggatgtgccatac 2502

Db     421 GAGCAGTTCCACCTTAAACACCCATTTCCTAGTAAACAGCAGCCAAAGGACGTGCCCTAC 480

Qy    2503 aaagaactcttaaagcagctgacttcccagcagcatgcgattcttattgaccttgggcga 2562

Db     481 AAAGAGCTCCTGAAGAAGCTGACCTCGCAGCAGCACGCCATTCTCATCGACCTCGGGCGA 540

Qy    2563 acctttcctacacacccatacttctctgcccagcttggagcaggacagctatcgctttac 2622

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Db     601 AACATTCTGAAGGCCTACTCGCTTCTGGACCAGGAGGTTGGATACTGCCAAGGTCTCAGC 660

Qy    2683 tttgtagcaggcattttgcttcttcatatgagtgaggaagaggcgtttaaaatgctcaag 2742

Db     661 TTTGTGGCAGGCATTTTGCTTCTTCACATGAGTGAGGAAGAGGCGTTCAAGATGCTCAAG 720

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Db     721 TTCCTGATGTTTGACATGGGGCTGCGGAAACAGTATCGGCCAGACATGATTATTTTGCAG 780

Qy    2803 atccagatgtaccagctctcgaggttgcttcatgattaccacagagacctctacaatcac 2862

Db     781 ATCCAGATGTACCAGCTGTCACGGCTCCTCCACGATTACCACCGAGACCTCTACAACCAC 840

Qy    2863 ctggaggagcacgagatcggcccccagcctctacgctgccccctggttcctcaccatgttt 2922

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Qy    2983 acagaggtcatatttaaagtggctttaagtctgttgggaagccataagcccttgattctg 3042

Db     961 TCAGAGGTCATATTTAAAGTAGCTTTAAGTCTTTTGGGGAGCCATAAGCCCTTGATTCTA 1020

Qy    3043 cagcatgaaaacctagaaaccatagttgactttataaaaagcacgctacccaaccttggc 3102

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Qy    3283 cttgacctccttgaacagttgcaggtggcaaatggtaggatccaaagccttgaggccacc 3342

Db    1261 CTTGACCTCCTGGAGCAGTTGCAGGTGGCAAATGCTAGGATCCAAAGCCTTGAAGCCACG 1320

Qy    3343 attgagaagctcctgagcagtgagagcaagctgaagcaggccatgcttaccttagaactg 3402

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Qy    3403 gagcggtcggccctgctgcagacggtggaggagctgcggcggcggagcgcagagcccagc 3462

Db    1381 GAGCGCTCCGCCCTGCTGCAGATGGTGGAGGAGCTGCGGAGGCAAAGCGCCCGGCCCAGC 1440

Qy    3463 gaccgggagcctgagtgcacgcagcccgagcccacgggcgactgacagct 3512

Db    1441 ACTCCAGAGCCAGACTGCACCCAGCTGGAGCCCACAGGCGATTGACCGCT 1490
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RESULT 8
AK057182
LOCUS AK057182 1788 bp mRNA linear PRI 31-OCT-2001
DEFINITION Homo sapiens cDNA FLJ32620 fis, clone STOMA2000386, highly similar to Bos taurus mRNA for lyncein.
ACCESSION AK057182
VERSION AK057182.1 GI:16552778
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens stomach cDNA to mRNA, clone_lib:STOMA2 clone:STOMA2000386.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Suzuki,O., Sasaki,N., Aotsuka,S., Shoji,T., Ichihara,T., Shiohata,N., Matsumoto,K., Hirano,M., Sano,S., Nomura,R., Yoshikawa,Y., Matsumura,Y., Moriya,S., Chiba,E., Momiyama,H., Onogawa,S., Kaeriyama,S., Satoh,N., Matsunawa,H., Takahashi,E., Kataoka,R., Kuga,N., Kuroda,A., Satoh,I., Kamata,K., Takami,S., Terashima,Y., Watanabe,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1788)
AUTHORS Isogai,T., Otsuki,T. and Sugiyama,T.
TITLE Direct Submission
JOURNAL Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952)
COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and HRI.
FEATURES Location/Qualifiers
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ACCESSION   AB011175
VERSION     AB011175.1  GI:3043729
KEYWORDS    KIAA0603 protein.
SOURCE      Homo sapiens male brain cDNA to mRNA, clone_lib:pBluescriptII SK
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  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 5922)
  AUTHORS   Ohara,O., Nagase,T. and Ishikawa,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-FEB-1998) Osamu Ohara, Kazusa DNA Research Institute,
            DNA Technology; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913,
            Fax:+81-438-52-3914)
REFERENCE   2  (sites)
  AUTHORS   Nagase,T., Ishikawa,K., Miyajima,N., Tanaka,A., Kotani,H.,
            Nomura,N. and Ohara,O.
  TITLE     Prediction of the coding sequences of unidentified human genes. IX.
            The complete sequences of 100 new cDNA clones from brain which can
            code for large proteins in vitro
  JOURNAL   DNA Res. 5 (1), 31-39 (1998)
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Query Match 19.2%; Score 682.2; DB 9; Length 5922;
Best Local Similarity 56.6%; Pred. No. 1.9e-138;
Matches 1585; Conservative 0; Mismatches 1028; Indels 186; Gaps 10;

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DT   03-JUL-2000 (Rel. 64, Last updated, Version 4)
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RT   "Homo sapiens chromosome 4, clone RP11-392K14";
RL   Unpublished.
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RA   Cerny J., Colangelo M., Collins S., Collymore A., Cooke P., DeArellano K.,
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RA   Riley R., Roberts D., Roy A., Severy P., Stange-Thomann N., Stojanovic N.,
RA   Stone C., Subramanian A., Tesfaye S., Torruella-Miller I., Vassiliev H.,
RA   Vo A., Wagner A., Wheeler J., Wu X., Wyman D., Ye W.J., Zody M.;
RT   ;
RL   Submitted (27-AUG-1999) to the EMBL/GenBank/DDBJ databases.
RL   Whitehead Institute/MIT Center for Genome Research, 320 Charles Street,
RL   Cambridge, MA 02141, USA
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CC   On Jun 23, 2000 this sequence version replaced gi:6006228.
CC   All repeats were identified using RepeatMasker:
CC   Smit, A.F.A. & Green, P. (1996-1997)
CC   http://ftp.genome.washington.edu/RM/RepeatMasker.html
CC   -------------- Genome Center
CC   Center: Whitehead Institute/ MIT Center for Genome Research
CC   Center code: WIBR
CC   Web site: http://www-seq.wi.mit.edu
CC   Contact: sequence_submissions@genome.wi.mit.edu
CC   -------------- Project Information
CC   Center project name: L1755
CC   Center clone name: 392_K_14
CC   -------------- Summary Statistics
CC   Sequencing vector: M13; M77815; 100% of reads
CC   Chemistry: Dye-primer-amersham; 5% of reads
CC   Chemistry: Dye-terminator Big Dye; 95% of reads
CC   Assembly program: Phrap; version 0.960731
CC   Consensus quality: 164704 bases at least Q40
CC   Consensus quality: 175594 bases at least Q30
CC   Consensus quality: 181024 bases at least Q20
CC   Insert size: 214000; agarose-fp
CC   Insert size: 187111; sum-of-contigs
CC   Quality coverage: 3.0 in Q20 bases; agarose-fp
CC   Quality coverage: 3.5 in Q20 bas.
CC   * NOTE: This is a 'working draft' sequence. It currently
CC   * consists of 28 contigs. The true order of the pieces
CC   * is not known and their order in this sequence record is
CC   * arbitrary. Gaps between the contigs are represented as
CC   * runs of N, but the exact sizes of the gaps are unknown.
CC   * This record will be updated with the finished sequence
CC   * as soon as it is available and the accession number will
CC   * be preserved.
CC   *        1      451: contig of 451 bp in length
CC   *      452 551: gap of      100 bp
CC   *      552     2663: contig of 2112 bp in length
CC   *     2664 2763: gap of      100 bp
CC   *     2764     4124: contig of 1361 bp in length
CC   *     4125 4224: gap of      100 bp
CC   *     4225     6767: contig of 2543 bp in length
CC   *     6768 6867: gap of      100 bp
CC   *     6868     8750: contig of 1883 bp in length
CC   *     8751 8850: gap of      100 bp
CC   *     8851    11272: contig of 2422 bp in length
CC   *    11273 11372: gap of      100 bp
CC   *    11373    13411: contig of 2039 bp in length
CC   *    13412 13511: gap of      100 bp
CC   *    13512    16962: contig of 3451 bp in length
CC   *    16963 17062: gap of      100 bp
CC   *    17063    22544: contig of 5482 bp in length
CC   *    22545 22644: gap of      100 bp
CC   *    22645    26284: contig of 3640 bp in length
CC   *    26285 26384: gap of      100 bp
```

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CC   *    26385    31223: contig of 4839 bp in length
CC   *    31224 31323: gap of     100 bp
CC   *    31324    36014: contig of 4691 bp in length
CC   *    36015 36114: gap of     100 bp
CC   *    36115    41939: contig of 5825 bp in length
CC   *    41940 42039: gap of     100 bp
CC   *    42040    48122: contig of 6083 bp in length
CC   *    48123 48222: gap of     100 bp
CC   *    48223    52983: contig of 4761 bp in length
CC   *    52984 53083: gap of     100 bp
CC   *    53084    58094: contig of 5011 bp in length
CC   *    58095 58194: gap of     100 bp
CC   *    58195    64606: contig of 6412 bp in length
CC   *    64607 64706: gap of     100 bp
CC   *    64707    71079: contig of 6373 bp in length
CC   *    71080 71179: gap of     100 bp
CC   *    71180    79886: contig of 8707 bp in length
CC   *    79887 79986: gap of     100 bp
CC   *    79987    86155: contig of 6169 bp in length
CC   *    86156 86255: gap of     100 bp
CC   *    86256    95370: contig of 9115 bp in length
CC   *    95371 95470: gap of     100 bp
CC   *    95471   103712: contig of 8242 bp in length
CC   *   103713 103812: gap of     100 bp
CC   *   103813   113565: contig of 9753 bp in length
CC   *   113566 113665: gap of     100 bp
CC   *   113666   123867: contig of 10202 bp in length
CC   *   123868 123967: gap of     100 bp
CC   *   123968   132296: contig of 8329 bp in length
CC   *   132297 132396: gap of     100 bp
CC   *   132397   141110: contig of 8714 bp in length
CC   *   141111 141210: gap of     100 bp
CC   *   141211   161622: contig of 20412 bp in length
CC   *   161623 161722: gap of     100 bp
CC   *   161723   189811: contig of 28089 bp in length.
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FH   Key             Location/Qualifiers
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FT   source          1. .189811
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FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /map="4"
FT                   /clone="RP11-392K14"
FT                   /clone_lib="RPCI-11 Human Male BAC"
FT   misc_feature    1. .451
FT                   /note="assembly_fragment clone_end:T7 vector_side:right"
FT   misc_feature    552. .2663
FT                   /note="assembly_fragment"
FT   misc_feature    2764. .4124
FT                   /note="assembly_fragment"
FT   misc_feature    4225. .6767
FT                   /note="assembly_fragment"
FT   misc_feature    6868. .8750
FT                   /note="assembly_fragment"
FT   misc_feature    8851. .11272
FT                   /note="assembly_fragment"
FT   misc_feature    11373. .13411
FT                   /note="assembly_fragment"
FT   misc_feature    13512. .16962
FT                   /note="assembly_fragment"
FT   misc_feature    17063. .22544
FT                   /note="assembly_fragment"
FT   misc_feature    22645. .26284
FT                   /note="assembly_fragment"
FT   misc_feature    26385. .31223
FT                   /note="assembly_fragment"
FT   misc_feature    31324. .36014
FT                   /note="assembly_fragment"
FT   misc_feature    36115. .41939
FT                   /note="assembly_fragment"
FT   misc_feature    42040. .48122
FT                   /note="assembly_fragment"
FT   misc_feature    48223. .52983
FT                   /note="assembly_fragment clone_end:SP6 vector_side:left"
FT   misc_feature    53084. .58094
FT                   /note="assembly_fragment"
FT   misc_feature    58195. .64606
FT                   /note="assembly_fragment"
FT   misc_feature    64707. .71079
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FT   misc_feature    71180. .79886
FT                   /note="assembly_fragment"
FT   misc_feature    79987. .86155
FT                   /note="assembly_fragment"
FT   misc_feature    86256. .95370
FT                   /note="assembly_fragment"
FT   misc_feature    95471. .103712
FT                   /note="assembly_fragment"
FT   misc_feature    103813. .113565
FT                   /note="assembly_fragment"
FT   misc_feature    113666. .123867
FT                   /note="assembly_fragment"
FT   misc_feature    123968. .132296
FT                   /note="assembly_fragment"
FT   misc_feature    132397. .141110
FT                   /note="assembly_fragment"
FT   misc_feature    141211. .161622
FT                   /note="assembly_fragment"
FT   misc_feature    161723. .189811
FT                   /note="assembly_fragment"
XX
SQ   Sequence 189811 BP; 52455 A; 40839 C; 40321 G; 53485 T; 2711 other;


  Query Match             13.1%;  Score 465.8;  DB 30;  Length 189811;
  Best Local Similarity   99.6%;  Pred. No. 5.2e-91;
  Matches  467;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    416 aagtgcctgagatcatcagctccatccgtcaggcggggaagatcgcccggcaggaggagc 475
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  97313 AGGTGCCTGAGATCATCAGCTCCATCCGTCAGGCGGGGAAGATCGCCCGGCAGGAGGAGC 97254

Qy    476 tgcactgcccgtccgagttcgacgacacgttttccaagaagttcgaggtgctcttctgcg 535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  97253 TGCACTGCCCGTCCGAGTTCGACGACACGTTTTCCAAGAAGTTCGAGGTGCTCTTCTGCG 97194

Qy    536 gccgcgtgacggtggcgcacaagaaggctccgccggccctgatcgacgagtgcatcgaga 595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  97193 GCCGCGTGACGGTGGCGCACAAGAAGGCTCCGCCGGCCCTGATCGACGAGTGCATCGAGA 97134

Qy    596 agttcaatcacgtcagcggcagccgggggtccgagagcccccgccccaacccgccccatg 655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  97133 AGTTCAATCACGTCAGCGGCAGCCGGGGGTCCGAGAGCCCCCGCCCCAACCCGCCCCATG 97074

Qy    656 ccgcgcccacagggagccaggagcctgtgcgcaggcccatgcgcaagtccttctcccagc 715
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Db  97073 CCGCGCCCACAGGGAGCCAGGAGCCTGTGCGCAGGCCCATGCGCAAGTCCTTCTCCCAGC 97014

Qy    716 ccggcctgcgctcgctggcctttaggaaggagctgcaggatgggggcctccgaagcagcg 775
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  97013 CCGGCCTGCGCTCGCTGGCCTTTAGGAAGGAGCTGCAGGATGGGGGCCTCCGAAGCAGCG 96954

Qy    776 gcttcttcagctccttcgaggagagcgacattgagaaccacctcattagcggacacaata 835
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  96953 GCTTCTTCAGCTCCTTCGAGGAGAGCGACATTGAGAACCACCTCATTAGCGGACACAATA 96894

Qy    836 ttgtgcagcccacagatatcgaggaaaatcgaactatgctcttcacgat 884
          |||||||||||||||||||||||||||||||||||||||||||||||| |
Db  96893 TTGTGCAGCCCACAGATATCGAGGAAAATCGAACTATGCTCTTCACGGT 96845


RESULT  11
AC021106
LOCUS       AC021106              195108 bp    DNA     linear   PRI 03-JUL-2001
DEFINITION  Homo sapiens clone RP11-177C12, complete sequence.
```

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ACCESSION   AC021106
VERSION     AC021106.6  GI:14589687
KEYWORDS    HTG.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 195108)
  AUTHORS   Waterston,R.H.
  TITLE     The sequence of Homo sapiens clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 195108)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-JAN-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   3  (bases 1 to 195108)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-JUL-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
COMMENT     On Jul 3, 2001 this sequence version replaced gi:14018126.

            ------------------- Genome Center --------------------
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site:http://genome.wustl.edu/gsc/index.shtml
            ---------------- Project Information -----------------
            Center project name: H_NH0177C12
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FEATURES             Location/Qualifiers
     source          1. .195108
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="RP11-177C12"
BASE COUNT    53372 a  40112 c  41873 g  59751 t
ORIGIN
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  Query Match           13.1%;  Score 465.8;  DB 9;  Length 195108;
  Best Local Similarity  99.6%;  Pred. No. 5.2e-91;
  Matches  467;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    416 aagtgcctgagatcatcagctccatccgtcaggcggggaagatcgcccggcaggaggagc 475
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 180759 AGGTGCCTGAGATCATCAGCTCCATCCGTCAGGCGGGGAAGATCGCCCGGCAGGAGGAGC 180818

Qy    476 tgcactgcccgtccgagttcgacgacacgttttccaagaagttcgaggtgctcttctgcg 535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 180819 TGCACTGCCCGTCCGAGTTCGACGACACGTTTTCCAAGAAGTTCGAGGTGCTCTTCTGCG 180878

Qy    536 gccgcgtgacggtggcgcacaagaaggctccgccggccctgatcgacgagtgcatcgaga 595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 180879 GCCGCGTGACGGTGGCGCACAAGAAGGCTCCGCCGGCCCTGATCGACGAGTGCATCGAGA 180938

Qy    596 agttcaatcacgtcagcggcagccgggggtccgagagcccccgccccaacccgccccatg 655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 180939 AGTTCAATCACGTCAGCGGCAGCCGGGGGTCCGAGAGCCCCCGCCCCAACCCGCCCCATG 180998

Qy    656 ccgcgcccacagggagccaggagcctgtgcgcaggcccatgcgcaagtccttctcccagc 715
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 180999 CCGCGCCCACAGGGAGCCAGGAGCCTGTGCGCAGGCCCATGCGCAAGTCCTTCTCCCAGC 181058

Qy    716 ccggcctgcgctcgctggcctttaggaaggagctgcaggatgggggcctccgaagcagcg 775
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181059 CCGGCCTGCGCTCGCTGGCCTTTAGGAAGGAGCTGCAGGATGGGGGCCTCCGAAGCAGCG 181118

Qy    776 gcttcttcagctccttccgaggagagcgacattgagaaccacctcattagcggacacaata 835
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Db 181119 GCTTCTTCAGCTCCTTCGAGGAGAGCGACATTGAGAACCACCTCATTAGCGGACACAATA 181178
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Qy    836 ttgtgcagcccacagatatcgaggaaaatcgaactatgctcttcacgat 884
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Db 181179 TTGTGCAGCCCACAGATATCGAGGAAAATCGAACTATGCTCTTCACGGT 181227
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RESULT  12
AC108933/c
LOCUS       AC108933              208318 bp    DNA     linear   HTG 01-FEB-2002
DEFINITION  Homo sapiens chromosome 4 clone RP11-392K14, WORKING DRAFT
            SEQUENCE, 5 unordered pieces.
ACCESSION   AC108933 AC009595
VERSION     AC108933.1  GI:18464316
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 208318)
  AUTHORS   Waterston,R.H.
  TITLE     The sequence of Homo sapiens clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 208318)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-FEB-2002) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
COMMENT     On Feb 1, 2002 this sequence version replaced gi:8671945.

            ------------------- Genome Center --------------------
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site:http://genome.wustl.edu/gsc/index.shtml
            Contact: submissions@watson.wustl.edu
            ---------------- Project Information -----------------
            Center project name: H_NH0392K14
            Drafting center: WIBR
            ------------------------------------------------------
            ------------- Summary Statistics  --------------
            Sequencing vector: M13; %
            Sequencing vector: plasmid; %
            Chemistry: Dye-primer ET; % of reads
            Chemistry: Dye-terminator Big Dye; % of reads
            Assembly program: Phrap; version 0.990319
            Consensus quality: 205652 bases at least Q40
            Consensus quality: 206608 bases at least Q30
            Consensus quality: 207022 bases at least Q20
            Insert size: 218000; agarose-fp
            Insert size: 207918; sum-of-contigs
            Quality coverage: 6.45 in Q20 bases; agarose-fp
            Quality coverage: 6.62 in Q20 bases; sum-of-contigs
            ------------------------------------------------------
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 5 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1    25746: contig of 25746 bp in length
            *    25747    25846: gap of unknown length
            *    25847    65131: contig of 39285 bp in length
            *    65132    65231: gap of unknown length
            *    65232   105028: contig of 39797 bp in length
            *   105029   105128: gap of unknown length
            *   105129   159307: contig of 54179 bp in length
            *   159308   159407: gap of unknown length
            *   159408   208318: contig of 48911 bp in length.
FEATURES             Location/Qualifiers
     source          1. .208318
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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                     /chromosome="4"
                     /clone="RP11-392K14"
     misc_feature    1. .25746
                     /note="assembly_name:Contig16"
     misc_feature    25847. .65131
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     misc_feature    65232. .105028
                     /note="assembly_name:Contig18"
     misc_feature    105129. .159307
                     /note="assembly_name:Contig19"
     misc_feature    159408. .208318
                     /note="assembly_name:Contig20"
BASE COUNT    59195 a  45373 c  44728 g  58621 t    401 others
ORIGIN


  Query Match             13.1%;  Score 465.8;  DB 2;  Length 208318;
  Best Local Similarity   99.6%;  Pred. No. 5.2e-91;
  Matches  467;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy     416 aagtgcctgagatcatcagctccatccgtcaggcggggaagatcgcccggcaggaggagc 475
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Db  129553 AGGTGCCTGAGATCATCAGCTCCATCCGTCAGGCGGGGAAGATCGCCCGGCAGGAGGAGC 129494

Qy     476 tgcactgcccgtccgagttcgacgacacgttttccaagaagttcgaggtgctcttctgcg 535
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  129493 TGCACTGCCCGTCCGAGTTCGACGACACGTTTTCCAAGAAGTTCGAGGTGCTCTTCTGCG 129434

Qy     536 gccgcgtgacggtggcgcacaagaaggctccgccggccctgatcgacgagtgcatcgaga 595
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Db  129433 GCCGCGTGACGGTGGCGCACAAGAAGGCTCCGCCGGCCCTGATCGACGAGTGCATCGAGA 129374

Qy     596 agttcaatcacgtcagcggcagccgggggtccgagagcccccgccccaacccgccccatg 655
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  129373 AGTTCAATCACGTCAGCGGCAGCCGGGGGTCCGAGAGCCCCCGCCCCAACCCGCCCCATG 129314

Qy     656 ccgcgcccacagggagccaggagcctgtgcgcaggcccatgcgcaagtccttctcccagc 715
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  129313 CCGCGCCCACAGGGAGCCAGGAGCCTGTGCGCAGGCCCATGCGCAAGTCCTTCTCCCAGC 129254

Qy     716 ccggcctgcgctcgctggcctttaggaaggagctgcaggatgggggcctccgaagcagcg 775
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Db  129253 CCGGCCTGCGCTCGCTGGCCTTTAGGAAGGAGCTGCAGGATGGGGGCCTCCGAAGCAGCG 129194

Qy     776 gcttcttcagctccttcgaggagagcgacattgagaaccacctcattagcggacacaata 835
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  129193 GCTTCTTCAGCTCCTTCGAGGAGAGCGACATTGAGAACCACCTCATTAGCGGACACAATA 129134

Qy     836 ttgtgcagcccacagatatcgaggaaaatcgaactatgctcttcacgat 884
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Db  129133 TTGTGCAGCCCACAGATATCGAGGAAAATCGAACTATGCTCTTCACGGT 129085


RESULT  13
AL390202_04/c
WPCOMMENT
  Sequence split into 10 fragments  LOCUS AL390202 Accession AL390202
     Fragment Name      Begin     End
     AL390202_00            1   110000
     AL390202_01       100001   210000
     AL390202_02       200001   310000
     AL390202_03       300001   410000
     AL390202_04       400001   510000
     AL390202_05       500001   610000
     AL390202_06       600001   710000
     AL390202_07       700001   810000
     AL390202_08       800001   910000
     AL390202_09       900001   988176
Continuation (5 of 10) of AL390202 from base 400001 (AL390202 Homo sapiens chromosome 20


  Query Match             11.9%;  Score 424.2;  DB 2;  Length 110000;
  Best Local Similarity   96.0%;  Pred. No. 6.1e-82;

  Matches  435;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy       1 atggaaccaataacattcacagcaaggaaacatctgcttcctaacgaggtctcggtggat 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   10365 ATGGAACCAATAACATTCACAGCAAGGAAACATCTGCTTCCTAACGAGGTCTCGGTGGAT 10306

Qy      61 tttggcctgcagctggtgggctccctgcctgtgcattccctgaccaccatgcccatgctg 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   10305 TTTGGCCTGCAGCTGGTGGGCTCCCTGCCTGTGCATTCCCTGACCACCATGCCCATGCTG 10246

Qy     121 ccctgggttgtggctgaggtgcgaagactcagcaggcagtccaccagaaaggaacctgta 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   10245 CCCTGGGTTGTGGCTGAGGTGCGAAGACTCAGCAGGCAGTCCACCAGAAAGGAACCTGTA 10186

Qy     181 accaagcaagtccggctttgcgtttcaccctctggactgagatgtgaacctgagccaggg 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   10185 ACCAAGCAAGTCCGGCTTTGCGTTTCACCCTCTGGACTGAGATGTGAACCTGAGCCAGGG 10126

Qy     241 agaagtcaacagtgggatcccctgatctattccagcatctttgagtgcaagcctcagcgt 300
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Db   10125 AGAAGTCAACAGTGGGATCCCCTGATCTATTCCAGCATCTTTGAGTGCAAGCCTCAGCGT 10066

Qy     301 gttcacaaactgattcacaacagtcatgacccaagttactttgcttgtctgattaaggaa 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   10065 GTTCACAAACTGATTCACAACAGTCATGACCCAAGTTACTTTGCTTGTCTGATTAAGGAA 10006

Qy     361 gacgctgtccaccggcagagtatctgctatgtgttcaaagccgatgatcaaacaaaaagtg 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   10005 GACGCTGTCCACCGGCAGAGTATCTGCTATGTGTTCAAAGCCGATGATCAAACAAAAGTA 9946

Qy     421 cctgagatcatcagctccatccgtcaggcgggg 453
             ||||||    | |   |    | ||| | ||
Db    9945 AGTGAGATGGAGATCCAAAAGACTAAGGTGTGG 9913


RESULT  14
DMU50542
LOCUS       DMU50542               3214 bp    mRNA    linear   INV 12-JUN-1996
DEFINITION  Drosophila melanogaster pollux (plx) mRNA, complete cds.
ACCESSION   U50542
VERSION     U50542.1  GI:1373162
KEYWORDS    .
SOURCE      fruit fly strain=Oregon R.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 3214)
  AUTHORS   Zhang,S.D., Kassis,J., Olde,B., Mellerick,D.M. and Odenwald,W.F.
  TITLE     Pollux, a novel Drosophila adhesion molecule, belongs to a family
            of proteins expressed in plants, yeast, nematodes, and man
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3214)
  AUTHORS   Zhang,S.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-MAR-1996) Shang-Ding Zhang, Neurogenetics, LNC,
            NINDS, NIH, 9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .3214
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                     /strain="Oregon R"
                     /db_xref="taxon:7227"
                     /chromosome="3"
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  AUTHORS   Xu,X.Z., Wes,P.D., Chen,H., Li,H.S., Yu,M., Morgan,S., Liu,Y. and
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  TITLE     Retinal targets for calmodulin include proteins implicated in
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  JOURNAL   J. Biol. Chem. 273 (47), 31297-31307 (1998)
  MEDLINE   99030403
REFERENCE   2  (bases 1 to 4746)
  AUTHORS   Montell,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-AUG-1998) C. Montell, The Johns Hopkins University
            School of Medicine, Department of Biological Chermistry, 725 N.
            Wolfe Street, Baltimore, MD 21205-2185, USA
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SUMMARIES

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ALIGNMENTS

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; Patent No. 5700927
; GENERAL INFORMATION:
; APPLICANT: Zon, Leonard and Richardson, Paul
; TITLE OF INVENTION: Tbc1 Gene and Uses Thereof
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,300
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04590/009001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4039 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 403..3829
US-08-363-300-1

Query Match 70.6%; Score 2510.4; DB 1; Length 4039;
Best Local Similarity 83.7%; Pred. No. 0;
Matches 2949; Conservative 0; Mismatches 536; Indels 37; Gaps 8;

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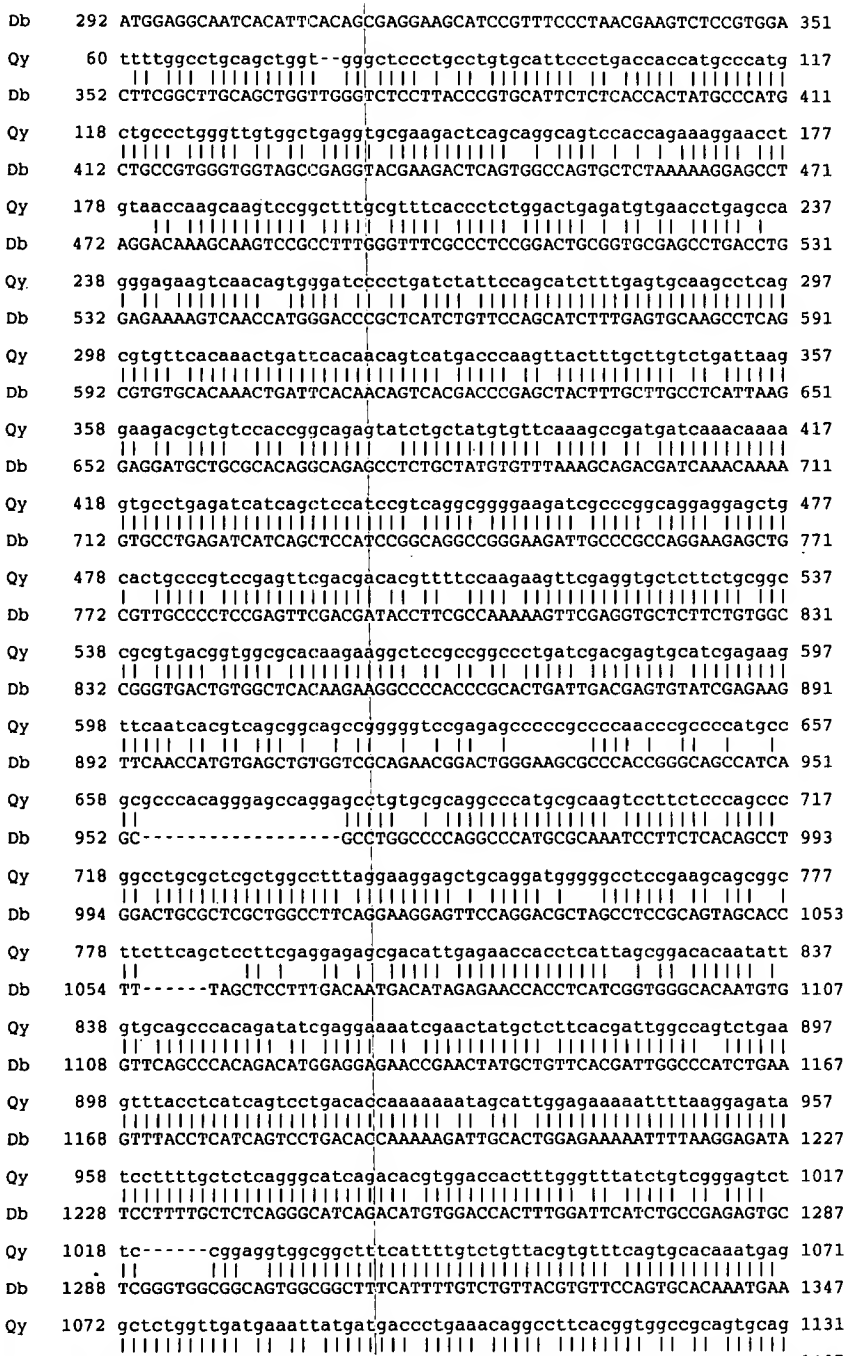
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Db   2487 GGAGAAGGAGAATCAGAAGCTACAAGCCTCTGAAAACGATTTGCTGAACAAACGCCTCAA 2546

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Db   2607 GCTTAGCACTCCAGGAAGATCCAAAATTAAGTTTGACATGGAAAAAGTGCACTCAGCTGT 2666

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Db   2667 TGGGCAAGGTGTGCCACGTCATCACCGAGGTGAGATCTGGAAATTTCTAGCTGAGCAGTT 2726

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RESULT 2
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
US-08-232-463-14

Query Match 1.6%; Score 57.8; DB 1; Length 7218;
Best Local Similarity 2.9%; Pred. No. 9.7e-06;
Matches 11; Conservative 225; Mismatches 147; Indels 0; Gaps 0;

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Qy   1438 attggaagtgaattaccacccagtgccactcgatttaggctagatatgctgaaaaacaaa 1497
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Qy   1498 gcaaagagatctttaacagagtctttagaaagtattttgtcccggggtaataaagccaga 1557
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RESULT   3
US-08-920-812-13
; Sequence 13, Application US/08920812
; Patent No. 5763188
;  GENERAL INFORMATION:
;    APPLICANT:  Ohno, Tsuneya
;    APPLICANT:  Matsuhisa, Akio
;    APPLICANT:  Uehara, Hirotsugu
;    APPLICANT:  Eda, Soji
;    TITLE OF INVENTION:  Probe for Diagnosing Infectious Disease
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/920,812
;      FILING DATE:  29-AUG-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/362,577
;      FILING DATE:  27-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rin-Laures, Li-Hsien
;      REGISTRATION NUMBER:  33,547
;      REFERENCE/DOCKET NUMBER:  19036/32420
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9515 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Pseudomonas aeruginosa
;      STRAIN:  Clinical Isolate P2-2
US-08-920-812-13


  Query Match             1.3%;  Score 45.4;  DB 1;  Length 9515;
  Best Local Similarity   46.2%;  Pred. No. 0.033;
  Matches  151;  Conservative    0;  Mismatches  176;  Indels    0;  Gaps    0;

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Db    862 CGCCTGGTATGCGGAAAGCCTCGACAAGCTCTACGACCAGGTCGCGCCGGCCGCCCAGCA 921

Qy    558 gaaggctccgccggccctgatcgacgagtgcatcgagaagttcaatcacgtcagcggcag 617
Db    922 GACCCTGGCCACCATTACCCGCGTGCCGCTGGGGGTGATCGGCGCGGTGGTGCCGTGGAA 981

Qy    618 ccgggggtccgagagcccccgccccaacccgccccatgccgcgcccacagggagccagga 677
Db    982 CTTCCCGCTCGACATGGCCGCCTGGAAGCTCGCCCCGGCCCTGGCCGCCGGCAACTCGGT 1041

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RESULT   4
US-08-920-827-13
; Sequence 13, Application US/08920827
; Patent No. 5770375
;  GENERAL INFORMATION:
;    APPLICANT:  Ohno, Tsuneya
;    APPLICANT:  Matsuhisa, Akio
;    APPLICANT:  Uehara, Hirotsugu
;    APPLICANT:  Eda, Soji
;    TITLE OF INVENTION:  Probe for Diagnosing Infectious Disease
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/920,827
;      FILING DATE:  29-AUG-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/362,577
;      FILING DATE:  27-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rin-Laures, Li-Hsien
;      REGISTRATION NUMBER:  33,547
;      REFERENCE/DOCKET NUMBER:  19036/32420
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  9515 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Pseudomonas aeruginosa
;      STRAIN:  Clinical Isolate P2-2
US-08-920-827-13


  Query Match             1.3%;  Score 45.4;  DB 1;  Length 9515;
  Best Local Similarity   46.2%;  Pred. No. 0.033;
  Matches  151;  Conservative    0;  Mismatches  176;  Indels    0;  Gaps    0;

Qy     438 catccgtcaggcggggaagatcgcccggcaggaggagctgcactgcccgtccgagttcga 497
           |||  |  || ||| || |  |||| || |    ||  | | | || |  || |  ||
Db     802 CATGGGCAAGCCGGTGATGGACGCCTGGAACATCGATGTACCCGGCGCCGCCCACGTCTT 861

Qy     498 cgacacgttttccaagaagttcgaggtgctcttctgcggccgcgtgacggtggcgcacaa 557
           || |  || | |  | |   ||||   ||||| |  |     || | |||  || ||  |
Db     862 CGCCTGGTATGCGGAAAGCCTCGACAAGCTCTACGACCAGGTCGCGCCGGCCGCCCAGCA 921

Qy     558 gaaggctccgccggccctgatcgacgagtgcatcgagaagttcaatcacgtcagcggcag 617
           ||      |  |          ||    |      | ||     |       ||     | |
Db     922 GACCCTGGCCACCATTACCCGCGTGCCGCTGGGGGTGATCGGCGCGGTGGTGCCGTGGAA 981

Qy     618 ccgggggtccgagagccccccgcccaaccgccccatgccgcgcccacagggagccagga 677
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Db     982 CTTCCCGCTCGACATGGCCGCCTGGAAGCTCGCCCCGGCCCTGGCCGCCGGCAACTCGGT 1041

Qy     678 gcctgtgcgcaggcccatgcgcaagtccttctcccagcccggcctgcgctcgctggcctt 737
           |    |      | ||  ||   | | ||||||   |   |||||  |  ||||||| |
Db    1042 GGTGCTCAAGCCGGCCGAGCAGTCGCCGTTCTCCGCCCTGCGCCTGGCCGAGCTGGCCCT 1101

Qy     738 taggaaggagctgcaggatgggggcct 764
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Db    1102 GGAGGCGGGGGTGCCGGAAGGCGTGCT 1128


RESULT   5
US-08-921-177-13
; Sequence 13, Application US/08921177
; Patent No. 5798211
;  GENERAL INFORMATION:
;    APPLICANT:  Ohno, Tsuneya
;    APPLICANT:  Matsuhisa, Akio
;    APPLICANT:  Uehara, Hirotsugu
;    APPLICANT:  Eda, Soji
;    TITLE OF INVENTION:  Probe for Diagnosing Infectious Disease
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/921,177
;      FILING DATE:  29-AUG-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/362,577
;      FILING DATE:  27-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rin-Laures, Li-Hsien
;      REGISTRATION NUMBER:  33,547
;      REFERENCE/DOCKET NUMBER:  19036/32420
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9515 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Pseudomonas aeruginosa
;      STRAIN:  Clinical Isolate P2-2
US-08-921-177-13


  Query Match             1.3%;  Score 45.4;  DB 1;  Length 9515;
  Best Local Similarity   46.2%;  Pred. No. 0.033;
  Matches  151;  Conservative    0;  Mismatches  176;  Indels    0;  Gaps    0;

Qy     438 catccgtcaggcggggaagatcgcccggcaggaggagctgcactgcccgtccgagttcga 497
           |||  |  || ||| || |  |||| || |    ||  | | | || |  || |  ||
Db     802 CATGGGCAAGCCGGTGATGGACGCCTGGAACATCGATGTACCCGGCGCCGCCCACGTCTT 861

Qy     498 cgacacgttttccaagaagttcgaggtgctcttctgcggccgcgtgacggtggcgcacaa 557
           || |  || | |  | |   ||||   ||||| |  |     || | |||  || ||  |
Db     862 CGCCTGGTATGCGGAAAGCCTCGACAAGCTCTACGACCAGGTCGCGCCGGCCGCCCAGCA 921

Qy     558 gaaggctccgccggccctgatcgacgagtgcatcgagaagttcaatcacgtcagcggcag 617
           ||      |  |          ||    |      | ||     |       ||     | |
Db     922 GACCCTGGCCACCATTACCCGCGTGCCGCTGGGGGTGATCGGCGCGGTGGTGCCGTGGAA 981

Qy     618 ccgggggtccgagagccccccgcccaaccgccccatgccgcgcccacagggagccagga 677
           |   |  |||  |   ||  |   || |  |||  |||  | || | || | |  ||
Db     982 CTTCCCGCTCGACATGGCCGCCTGGAAGCTCGCCCCGGCCCTGGCCGCCGGCAACTCGGT 1041

Qy     678 gcctgtgcgcaggcccatgcgcaagtccttctcccagcccggcctgcgctcgctggcctt 737
           |    |      | ||  ||   | | ||||||   |   |||||  |  ||||||| |
Db    1042 GGTGCTCAAGCCGGCCGAGCAGTCGCCGTTCTCCGCCCTGCGCCTGGCCGAGCTGGCCCT 1101

Qy     738 taggaaggagctgcaggatgggggcct 764
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Db    1102 GGAGGCGGGGGTGCCGGAAGGCGTGCT 1128


RESULT   6
US-08-362-577C-13
; Sequence 13, Application US/08362577C
; Patent No. 5807673
;  GENERAL INFORMATION:
;    APPLICANT:  Ohno, Tsuneya
;    APPLICANT:  Matsuhisa, Akio
;    APPLICANT:  Uehara, Hirotsugu
;    APPLICANT:  Eda, Soji
;    TITLE OF INVENTION:  Probe for Diagnosing Infectious Disease
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/362,577C
;      FILING DATE:  27-MAR-1995
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;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rin-Laures, Li-Hsien
;      REGISTRATION NUMBER:  33,547
;      REFERENCE/DOCKET NUMBER:  19036/32420
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9515 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Pseudomonas aeruginosa
;      STRAIN:  Clinical Isolate P2-2
US-08-362-577C-13


  Query Match             1.3%;  Score 45.4;  DB 1;  Length 9515;
  Best Local Similarity   46.2%;  Pred. No. 0.033;
  Matches  151;  Conservative    0;  Mismatches  176;  Indels    0;  Gaps    0;

Qy    438 catccgtcaggcggggaagatcgcccggcaggaggagctgcactgcccgtccgagttcga 497
          |||  |  || ||| || |  |||| || |    ||  | | | || |  || |  ||
Db    802 CATGGGCAAGCCGGTGATGGACGCCTGGAACATCGATGTACCCGGCGCCGCCCACGTCTT 861

Qy    498 cgacacgttttccaagaagttcgaggtgctcttctgcggccgcgtgacggtggcgcacaa 557
          || |  || | |  | |   ||||   ||||| |  |     || | ||| || ||  |
Db    862 CGCCTGGTATGCGGAAAGCCTCGACAAGCTCTACGACCAGGTCGCGCCGGCCGCCCAGCA 921

Qy    558 gaaggctccgccggccctgatcgacgagtgcatcgagaagttcaatcacgtcagcggcag 617
          ||       |  |          ||    |       | ||    |      ||     | |
Db    922 GACCCTGGCCACCATTACCCGCGTGCCGCTGGGGGTGATCGGCGCGGTGGTGCCGTGGAA 981

Qy    618 ccgggggtccgagagcccccgccccaacccgccccatgccgcgcccacagggagccagga 677
          |    |  ||| |  ||  | | || |  ||| ||| | || | || | | ||
Db    982 CTTCCCGCTCGACATGGCCGCCTGGAAGCTCGCCCCGGCCCTGGCCGCCGGCAACTCGGT 1041

Qy    678 gcctgtgcgcaggcccatgcgcaagtccttctcccagcccggcctgcgctcgctggcctt 737
          |   |     | ||  ||   | | ||||||   |   |||||  |  |||||||  |
Db   1042 GGTGCTCAAGCCGGCCGAGCAGTCGCCGTTCTCCGCCCTGCGCCTGGCCGAGCTGGCCCT 1101

Qy    738 taggaaggagctgcaggatgggggcct 764
            |  || | ||| ||| || |  ||
Db   1102 GGAGGCGGGGGTGCCGGAAGGCGTGCT 1128


RESULT   7
US-08-920-828-13
; Sequence 13, Application US/08920828
; Patent No. 5853998
;  GENERAL INFORMATION:
;    APPLICANT:  Ohno, Tsuneya
;    APPLICANT:  Matsuhisa, Akio
;    APPLICANT:  Uehara, Hirotsugu
;    APPLICANT:  Eda, Soji
;    TITLE OF INVENTION:  Probe for Diagnosing Infectious Disease
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/920,828
;      FILING DATE:  29-AUG-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/362,577
;      FILING DATE:  27-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rin-Laures, Li-Hsien
;      REGISTRATION NUMBER:  33,547
;      REFERENCE/DOCKET NUMBER:  19036/32420
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9515 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Pseudomonas aeruginosa
;      STRAIN:  Clinical Isolate P2-2
US-08-920-828-13


  Query Match             1.3%;  Score 45.4;  DB 2;  Length 9515;
  Best Local Similarity   46.2%;  Pred. No. 0.033;
  Matches  151;  Conservative    0;  Mismatches  176;  Indels    0;  Gaps    0;

Qy    438 catccgtcaggcggggaagatcgcccggcaggaggagctgcactgcccgtccgagttcga 497
          |||  |  || ||| || |  |||| || |    ||  | | | || |  || |  ||
Db    802 CATGGGCAAGCCGGTGATGGACGCCTGGAACATCGATGTACCCGGCGCCGCCCACGTCTT 861

Qy    498 cgacacgttttccaagaagttcgaggtgctcttctgcggccgcgtgacggtggcgcacaa 557
          || |  || | |  | |   ||||   ||||| |  |     || | ||| || ||  |
Db    862 CGCCTGGTATGCGGAAAGCCTCGACAAGCTCTACGACCAGGTCGCGCCGGCCGCCCAGCA 921

Qy    558 gaaggctccgccggccctgatcgacgagtgcatcgagaagttcaatcacgtcagcggcag 617
          ||       |  |          ||    |       | ||    |      ||     | |
Db    922 GACCCTGGCCACCATTACCCGCGTGCCGCTGGGGGTGATCGGCGCGGTGGTGCCGTGGAA 981

Qy    618 ccgggggtccgagagcccccgccccaacccgccccatgccgcgcccacagggagccagga 677
          |    |  ||| |  ||  | | || |  ||| ||| | || | || | | ||
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Qy    678 gcctgtgcgcaggcccatgcgcaagtccttctcccagcccggcctgcgctcgctggcctt 737
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Qy    738 taggaaggagctgcaggatgggggcct 764
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Db   1102 GGAGGCGGGGGTGCCGGAAGGCGTGCT 1128


RESULT   8
US-08-253-155A-9
; Sequence 9, Application US/08253155A
; Patent No. 5691147
;  GENERAL INFORMATION:
;    APPLICANT:  Gyuris, Jeno
;    APPLICANT:  Draetta, Giulio
;    TITLE OF INVENTION:  CDK4 Binding Proteins
;    NUMBER OF SEQUENCES:  95
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
```

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;       ZIP:  02109
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  ASCII(text)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/253,155A
;       FILING DATE:  02-JUN-1994
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Vincent, Matthew P.
;       REGISTRATION NUMBER:  36,709
;       REFERENCE/DOCKET NUMBER:  MII-028
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617) 227-7400
;       TELEFAX:  (617) 227-5941
;   INFORMATION FOR SEQ ID NO:  9:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  8201 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-08-253-155A-9


  Query Match             1.3%;  Score 45;  DB 1;  Length 8201;
  Best Local Similarity   53.0%;  Pred. No. 0.039;
  Matches   96;  Conservative    0;  Mismatches   85;  Indels    0;  Gaps    0;

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           | ||| |  ||  ||  | | |  ||    | |||    |  |    ||||||   |
Db    2133 TGGACGTGAGGACGACTCTCCGGAACCATGTCTTCTTTAGGGATCGATATGGAGCCAAGC 2192

Qy    2609 agctatcgctttacaacattttgaaggcctactcacttctagaccaggaagtgggatatt 2668
           ||     || | | ||||  |   |||||| ||        ||| ||| ||||| || |
Db    2193 AGAGGGAACTATTCTACATCCTCCTGGCCTATTCGGAGTATAACCCGGAGGTGGGCTACT 2252

Qy    2669 gccaaggtctcagctttgtagcaggcattttgcttcttcatatgagtgaggaagaggcgt 2728
           ||   |  || |||    |  | | | | || || ||| || ||  |||||| || || |
Db    2253 GCAGGGACCTGAGCCACATCACCGCCTTGTTCCTCCTTTATCTGCCTGAGGAGGACGCAT 2312

Qy    2729 t 2729
           |
Db    2313 T 2313


RESULT   9
US-08-295-060-3
; Sequence 3, Application US/08295060
; Patent No. 5659123
;  GENERAL INFORMATION:
;    APPLICANT:  VAN RIE, Jeroen
;    APPLICANT:  JANSENS, Stefan
;    APPLICANT:  PERFEROEN, Marnix
;    TITLE OF INVENTION:  NEW DIABROTICA TOXINS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  P.O. Box 1404
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  United States
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/295,060
;      FILING DATE:  26-AUG-1994
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Crane-Feury, Sharon E
;      REGISTRATION NUMBER:  36,113
;      REFERENCE/DOCKET NUMBER:  010830-052
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 836-6620
;      TELEFAX:  (703) 836-2021
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1957 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  13..1947
US-08-295-060-3


  Query Match             1.2%;  Score 41;  DB 1;  Length 1957;
  Best Local Similarity   47.9%;  Pred. No. 0.22;
  Matches  113;  Conservative    0;  Mismatches  123;  Indels    0;  Gaps    0;

Qy     488 ccgagttcgacgacacgttttccaagaagttcgaggtgctcttctgcggccgcgtgacgg 547
           || ||  | ||||||       |||   |  ||  |||  ||    | ||  ||    |
Db    1322 CCCAGACCTACGACAGCNNNCGCAACGTGGGCGCTGTGAGCTGGGACAGCATCGACCAGC 1381

Qy     548 tggcgcacaagaaggctccgccggccctgatcgacgagtgcatcgagaagttcaatcacg 607
           || | | |||    |      | |||||    | |  | || | |  || | ||  |||
Db    1382 TGCCTCCCGAGACCACCGACGAGCCCCTGGAGAAGGGCTACAGCCACCAGCTGAACTACG 1441

Qy     608 tcagcggcagccgggggtccgagagcccccgccccaacccgccccatgccgcgcccacag 667
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Db    1442 TGATGTGCTTCCTGATGCAGGGCAGCAGGGGCACCATCCCAGTGCTGACCTGGACCCACA 1501

Qy     668 ggagccaggagcctgtgcgcaggcccatgcgcaagtccttctcccagcccggcctg 723
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Db    1502 AGAGCGTGGACTTCTTCAACATGATCGACAGCAAGAAGATCACCCAGCTGCCCCTG 1557


RESULT  10
US-08-858-003-2
; Sequence 2, Application US/08858003
; Patent No. 6060234
;  GENERAL INFORMATION:
;    APPLICANT:  Katz, Leonard
;    APPLICANT:  Stassi, Diane L.
;    APPLICANT:  Summers Jr., Richard G.
;    APPLICANT:  Ruan, Xiaoan
;    APPLICANT:  Pereda-Lopez, Ana
;    APPLICANT:  Kakavas, Stephan J.
;    TITLE OF INVENTION:  NOVEL POLYKETIDE DERIVATIVES
;    TITLE OF INVENTION:  AND RECOMBINANT METHODS FOR MAKING SAME
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories
;      STREET:  100 Abbott Park Rd.
;      CITY:  Abbott Park
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60064-3500
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/858,003
;      FILING DATE:  16-MAY-1979
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;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dianne Casuto
;      REGISTRATION NUMBER:  P-40,943
;      REFERENCE/DOCKET NUMBER:  4952.US.P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (847)-938-3137
;      TELEFAX:  (847)-938-2623
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1030 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-858-003-2


  Query Match             1.1%;  Score 40.8;  DB 3;  Length 1030;
  Best Local Similarity   50.0%;  Pred. No. 0.18;
  Matches  102;  Conservative    0;  Mismatches  102;  Indels    0;  Gaps    0;

Qy    440 tccgtcaggcggggaagatcgcccggcaggaggagctgcactgcccgtccgagttcgacg 499
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Db    203 TCACACAGGCGGCTCTGTTCGCCGTGGAGACCTCCCTGTTCCGGCTGTTCGAGGCCCACG 262

Qy    500 acacgttttccaagaagttcgaggtgctcttctgcggccgcgtgacggtggcgcacaaga 559
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Db    263 GCCTCGTCCCCGACTACCTCATCGGCCACTCCATCGGCGAAGTGACCGCGGCCCACCTGG 322

Qy    560 aggctccgccggccctgatcgacgagtgcatcgagaagttcaatcacgtcagcggcagcc 619
            |     |  |  |||   |||| |||| ||  |     | | | || | ||   |  |
Db    323 CCGGGGTCCTCGATCTGGCGGACGCGTGCGTCCTGGTCGCCCACCGCGGCCGCCTGATGC 382

Qy    620 gggggtccgagagcccccgcccca 643
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Db    383 AGTCGGCCCGGGCCGGCGGCGCGA 406


RESULT  11
US-09-078-166-2
; Sequence 2, Application US/09078166
; Patent No. 6063561
;  GENERAL INFORMATION:
;    APPLICANT:  Katz, Leonard
;    APPLICANT:  Stassi, Diane L.
;    APPLICANT:  Summers Jr., Richard G.
;    APPLICANT:  Ruan, Xiaoan
;    APPLICANT:  Pereda-Lopez, Ana
;    APPLICANT:  Kakavas, Stephan J.
;    TITLE OF INVENTION:  NOVEL POLYKETIDE DERIVATIVES
;    TITLE OF INVENTION:  AND RECOMBINANT METHODS FOR MAKING SAME
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories
;      STREET:  100 Abbott Park Rd.
;      CITY:  Abbott Park
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60064-3500
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/078,166
;      FILING DATE:  16-MAY-1979
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dianne Casuto
;      REGISTRATION NUMBER:  P-40,943
;      REFERENCE/DOCKET NUMBER:  4952.US.P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (847)-938-3137
;      TELEFAX:  (847)-938-2623
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1030 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-09-078-166-2


  Query Match             1.1%;  Score 40.8;  DB 3;  Length 1030;
  Best Local Similarity   50.0%;  Pred. No. 0.18;
  Matches  102;  Conservative    0;  Mismatches  102;  Indels    0;  Gaps    0;

Qy    440 tccgtcaggcggggaagatcgcccggcaggaggagctgcactgcccgtccgagttcgacg 499
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Db    203 TCACACAGGCGGCTCTGTTCGCCGTGGAGACCTCCCTGTTCCGGCTGTTCGAGGCCCACG 262

Qy    500 acacgttttccaagaagttcgaggtgctcttctgcggccgcgtgacggtggcgcacaaga 559
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Db    263 GCCTCGTCCCCGACTACCTCATCGGCCACTCCATCGGCGAAGTGACCGCGGCCCACCTGG 322

Qy    560 aggctccgccggccctgatcgacgagtgcatcgagaagttcaatcacgtcagcggcagcc 619
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Db    323 CCGGGGTCCTCGATCTGGCGGACGCGTGCGTCCTGGTCGCCCACCGCGGCCGCCTGATGC 382

Qy    620 gggggtccgagagcccccgcccca 643
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Db    383 AGTCGGCCCGGGCCGGCGGCGCGA 406


RESULT  12
US-08-997-467-2
; Sequence 2, Application US/08997467
; Patent No. 6200813
;  GENERAL INFORMATION:
;    APPLICANT:  Katz, Leonard
;    APPLICANT:  Stassi, Diane L.
;    APPLICANT:  Summers Jr., Richard G.
;    APPLICANT:  Ruan, Xiaoan
;    APPLICANT:  Pereda-Lopez, Ana
;    APPLICANT:  Kakavas, Stephan J.
;    TITLE OF INVENTION:  NOVEL POLYKETIDE DERIVATIVES
;    TITLE OF INVENTION:  AND RECOMBINANT METHODS FOR MAKING SAME
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories
;      STREET:  100 Abbott Park Rd.
;      CITY:  Abbott Park
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60064-3500
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/997,467
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/858,003
;      FILING DATE:  16-MAY-1997
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;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dianne Casuto
;      REGISTRATION NUMBER:  P-40,943
;      REFERENCE/DOCKET NUMBER:  4952.US.P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (847)-938-3137
;      TELEFAX:  (847)-938-2623
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1030 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-997-467-2


  Query Match             1.1%;  Score 40.8;  DB 4;  Length 1030;
  Best Local Similarity   50.0%;  Pred. No. 0.18;
  Matches  102;  Conservative    0;  Mismatches  102;  Indels    0;  Gaps    0;

Qy    440 tccgtcaggcggggaagatcgcccggcaggaggagctgcactgcccgtccgagttcgacg 499
          ||   |||||||    | |||||  | ||      |||  | | | || ||||  | |||
Db    203 TCACACAGGCGGCTCTGTTCGCCGTGGAGACCTCCCTGTTCCGGCTGTTCGAGGCCCACG 262

Qy    500 acacgttttccaagaagttcgaggtgctcttctgcggccgcgtgacggtggcgcacaaga 559
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Db    263 GCCTCGTCCCCGACTACCTCATCGGCCACTCCATCGGCGAAGTGACCGCGGCCCCACCTGG 322

Qy    560 aggctccgccggccctgatcgacgagtgcatcgagaagttcaatcacgtcagcggcagcc 619
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Db    323 CCGGGGTCCTCGATCTGGCGGACGCGTGCGTCCTGGTCGCCCACCGCGGCCGCCTGATGC 382

Qy    620 gggggtccgagagccccccgcccca 643
            |  | ||  |  |  | || | |
Db    383 AGTCGGCCCGGGCCGGCGGCGCGA 406


RESULT  13
US-08-814-052-19
; Sequence 19, Application US/08814052
; Patent No. 6015783
;  GENERAL INFORMATION:
;    APPLICANT:  von der Osten, Claus
;    APPLICANT:  Cherry, Joel R.
;    APPLICANT:  Bjornvad, Mads E.
;    APPLICANT:  Vind, Jesper
;    APPLICANT:  Rasmussen, Michael Dolberg
;    TITLE OF INVENTION:  PROCESS FOR REMOVAL OR BLEACHING OF SOILING
;    TITLE OF INVENTION:  OR STAINS FROM CELLULOSIC FABRIC
;    NUMBER OF SEQUENCES:  55
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 6015783o No. 6015783disk of No. 6015783th America, Inc.
;      STREET:  405 Lexington Avenue, Suite 6400
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10174-6401
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/814,052
;      FILING DATE:  06-MAR-1997
;      CLASSIFICATION:  510
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lambiris, Elias J
;      REGISTRATION NUMBER:  33,728
;      REFERENCE/DOCKET NUMBER:  4684.204-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-867-0123
;      TELEFAX:  212-878-9655
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2249 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-814-052-19


  Query Match             1.1%;  Score 40.6;  DB 3;  Length 2249;
  Best Local Similarity   48.9%;  Pred. No. 0.31;
  Matches  109;  Conservative    0;  Mismatches  114;  Indels    0;  Gaps    0;

Qy    474 gctgcactgcccgtccgagttcgacgacacgttttccaagaagttcgaggtgctcttctg 533
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Db   1234 GCTCTGCGGCGGCTCCAGGAATCCCTACCCGGCCGCCATCTTCCACTACGCCGGCGCCCC 1293

Qy    534 cggccgcgtgacggtggcgcacaagaaggctccgccggccctgatcgacgagtgcatcga 593
          |||| ||  | |   ||   |   ||||| |||   | ||  | |  |  |  | ||
Db   1294 CGGCGGCCCGCCCACGGACGAGGGCAAGGCCCCGGTCGACCACAACTGCCTGGACCTCCC 1353

Qy    594 gaagttcaatcacgtcagcggcagccgggggtccgagagcccccgccccaacccgcccca 653
            ||  |||| | ||||   | | ||   | | ||  ||||   |  | |||| | |||| |
Db   1354 CAACCTCAAGCCCGTCGTGGCCCGCGACGTGCCCCTGAGCGGCTTCGCCAAGCGGCCCGA 1413

Qy    654 tgccgcgcccacagggagccaggagcctgtgcgcaggcccatg 696
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Db   1414 CAACACGCTCGACGTCACCCTCGACACCACGGGCACGCCCCTG 1456


RESULT  14
US-08-814-052-17
; Sequence 17, Application US/08814052
; Patent No. 6015783
;  GENERAL INFORMATION:
;    APPLICANT:  von der Osten, Claus
;    APPLICANT:  Cherry, Joel R.
;    APPLICANT:  Bjornvad, Mads E.
;    APPLICANT:  Vind, Jesper
;    APPLICANT:  Rasmussen, Michael Dolberg
;    TITLE OF INVENTION:  PROCESS FOR REMOVAL OR BLEACHING OF SOILING
;    TITLE OF INVENTION:  OR STAINS FROM CELLULOSIC FABRIC
;    NUMBER OF SEQUENCES:  55
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 6015783o No. 6015783disk of No. 6015783th America, Inc.
;      STREET:  405 Lexington Avenue, Suite 6400
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10174-6401
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/814,052
;      FILING DATE:  06-MAR-1997
;      CLASSIFICATION:  510
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lambiris, Elias J
;      REGISTRATION NUMBER:  33,728
;      REFERENCE/DOCKET NUMBER:  4684.204-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-867-0123
;      TELEFAX:  212-878-9655
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2279 base pairs
;      TYPE:  nucleic acid
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;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-814-052-17


  Query Match             1.1%;  Score 40.6;  DB 3;  Length 2279;
  Best Local Similarity   48.9%;  Pred. No. 0.32;
  Matches  109;  Conservative    0;  Mismatches  114;  Indels    0;  Gaps    0;

Qy     474 gctgcactgcccgtccgagttcgacgacacgttttccaagaagttcgaggtgctcttctg 533
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Db    1340 GCTCTGCGGCGGCTCCAGGAATCCCTACCCGGCCGCCATCTTCCACTACGCCGGCGCCCC 1399

Qy     534 cggccgcgtgacggtggcgcacaagaaggctccgccggccctgatcgacgagtgcatcga 593
           ||||  ||  | |   ||   |   ||||| |||   | ||  | |  |  |  |  | ||
Db    1400 CGGCGGCCCGCCCACGGACGAGGGCAAGGCCCCGGTCGACCACAACTGCCTGGACCTCCC 1459

Qy     594 gaagttcaatcacgtcagcggcagccgggggtccgagagcccccgccccaacccgcccca 653
            ||  |||| | ||||   | | ||   | | ||  ||||  |  | |||| | |||| |
Db    1460 CAACCTCAAGCCCGTCGTGGCCCGCGACGTGCCCCTGAGCGGCTTCGCCAAGCGGCCCGA 1519

Qy     654 tgccgcgcccacagggagccaggagcctgtgcgcaggcccatg 696
             | ||| |   |  | ||  ||  |   | ||| |||| ||
Db    1520 CAACACGCTCGACGTCACCCTCGACACCACGGGCACGCCCCTG 1562


RESULT  15
US-08-814-052-18
; Sequence 18, Application US/08814052
; Patent No. 6015783
;  GENERAL INFORMATION:
;    APPLICANT:  von der Osten, Claus
;    APPLICANT:  Cherry, Joel R.
;    APPLICANT:  Bjornvad, Mads E.
;    APPLICANT:  Vind, Jesper
;    APPLICANT:  Rasmussen, Michael Dolberg
;    TITLE OF INVENTION:  PROCESS FOR REMOVAL OR BLEACHING OF SOILING
;    TITLE OF INVENTION:  OR STAINS FROM CELLULOSIC FABRIC
;    NUMBER OF SEQUENCES:  55
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 6015783o No. 6015783disk of No. 6015783th America, Inc.
;      STREET:  405 Lexington Avenue, Suite 6400
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10174-6401
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/814,052
;      FILING DATE:  06-MAR-1997
;      CLASSIFICATION:  510
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lambiris, Elias J
;      REGISTRATION NUMBER:  33,728
;      REFERENCE/DOCKET NUMBER:  4684.204-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-867-0123
;      TELEFAX:  212-878-9655
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2300 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-814-052-18


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  Matches  109;  Conservative    0;  Mismatches  114;  Indels    0;  Gaps    0;

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           |||   | ||   |||  |    | || ||    |||       | | |    |  |
Db    1234 GCTCTGCGGCGGCTCCAGGAATCCCTACCCGGCCGCCATCTTCCACTACGCCGGCGCCCC 1293

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           ||||  ||  | |   ||   |   ||||| |||   | ||  | |  |  |  |  | ||
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Qy     594 gaagttcaatcacgtcagcggcagccgggggtccgagagcccccgccccaacccgcccca 653
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Db    1354 CAACCTCAAGCCCGTCGTGGCCCGCGACGTGCCCCTGAGCGGCTTCGCCAAGCGGCCCGA 1413

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Db    1414 CAACACGCTCGACGTCACCCTCGACACCACGGGCACGCCCCTG 1456


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GenCore version 4.5

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Run on: September 9, 2002, 14:07:12 ; Search time 5191.84 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
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10: gb_est2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	9	722.2	20.3	952	10	BE299948	BE299948 600944494
	10	713.8	20.1	838	10	BI907513	BI907513 603065640
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	14	683.4	19.2	754	10	BE300005	BE300005 600944594
	15	682.6	19.2	892	10	BE561889	BE561889 601346094
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	25	659.2	18.5	672	10	BE675153	BE675153 7f03d07.x
	26	652.8	18.4	806	9	AW043925	AW043925 wy82b07.x
	27	648.8	18.3	665	9	AW173375	AW173375 xj78g07.x
	28	647.8	18.2	812	10	BI758489	BI758489 603023334
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	35	630	17.7	722	10	BE560392	BE560392 601347108
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ALIGNMENTS

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LOCUS Z78359 1001 bp mRNA linear EST 28-JUL-1999
DEFINITION HSZ78359 Human fetal brain S. Meier-Ewert Homo sapiens cDNA clone 3.114 (CEPH) 5', mRNA sequence.
ACCESSION Z78359
VERSION Z78359.1 GI:1495132
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1001)
AUTHORS Neri,C., Albanese,V., Lebre,A.S., Holbert,S., Saada,C., Bougueleret,L., Meier-Ewert,S., LeGall,I., Millasseau,P., Bui,H., Giudicelli,C., Massart,C., Guillou,S., Gervy,P., Poullier,E., Rigault,P., Weissenbach,J., Lennon,G., Chumakov,I., Dausset,J., Lehrach,H., Cohen,D. and Cann,H.M.
TITLE Survey of CAG/CTG repeats in human cDNAs representing new genes: candidates for inherited neurological disorders
JOURNAL Hum. Mol. Genet. 5 (7), 1001-1009 (1996)
MEDLINE 96414310
COMMENT Contact: Neri C.
Fondation Jean Dausset - CEPH
27 Rue Juliette Dodu, 75010 Paris, France
Related sequence: Z78360
5'-sequence (upper strand).
FEATURES Location/Qualifiers
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/clone="3.114 (CEPH)"
/clone_lib="Human fetal brain S. Meier-Ewert"
/tissue_type="brain"
/dev_stage="fetus"
/note="cDNA library of S. Meier-Ewert, Max Planck Inst.f.Mol.Genetics, Berlin, FRG"
BASE COUNT 237 a 229 c 231 g 272 t 32 others
ORIGIN

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  Query Match           23.4%;  Score 833.6;  DB 10;  Length 1001;
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  Matches  937;  Conservative    0;  Mismatches   56;  Indels    9;  Gaps    8;

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Db   1001 ACATCTCGTGAGCTCCGAGAGCTGTGCCTAAAGGCTATTCTTCAACAGATNCTGCTGCTN 942

Qy   2206 agaatggagaaggaaaatcagaagctccaagcctctgaaaatgatttgctgaacaagcgc 2265
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Db    941 AGAATGGAGAAGGAAAATCAGAAGCTCCAAGCCTCTGAAAATGATTTGCTGAACAAGCGC 882

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Db    881 CTGAAGCTCGATTATGAAGAAATNACTCCCTGTCTTAAAGAAGTAACTACAGTGTGGGAA 822

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Db    821 AAGATGCTTAGCACTCCAGGAAGATCCCANAAATTAAGTTTGACATGGAAAAAATGCACT 762

Qy   2384 cggctgttgggc-aaggtgtgccacgtcatcaccgaggtgaaatctggaaa-tttctagc 2441
          || |||||||| |||||||||||||||||||||||||||||||||||||| ||||||||
Db    761 CGACTGTTGGGCTAAGGTGTGCCACGTCATCACCGAGGTGAAATCTGGAAATTTTCTAGC 702

Qy   2442 tgagcaa-ttccaccttaaacaccagtttcccagcaaacagcagccaaaggatgtgccat 2500
          ||||||| ||||||| |||||||||||||||||| |||||||||| ||||||||||||
Db    701 TGAGCAATTTCCACCGTAAACACCAGTTTCCCAGCANACAGCAGCCANAGGATGTGCCAT 642

Qy   2501 acaaagaactcttaaagcagctgacttcccagcagcatgcgattcttattgaccttgggc 2560
          |||||||||||| |||||||||||||||||||||||||||||||||||||||||||| |
Db    641 ACAAAGAACTCTTNAAGCAGCTGACTTCCCAGCAGCATGCGATTCTTATTGACCTTGGNC 582

Qy   2561 gaacctttcctacacacccatacttctctgcccagcttggagcaggacagctatcgcttt 2620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    581 GAACCTTTCCTACACACCCATACTTCTCTGCCCAGCTTGGAGCAGGACAGCTATCGCTTT 522

Qy   2621 acaacattttgaaggcctactcacttctagaccaggaagtgggatattgccaaggtctca 2680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    521 ACAACATTTTGAAGGCCTACTCACTTCTAGACCAGGAAGTGGGATATTGCCAAGGTCTCA 462

Qy   2681 gctttgtagcaggcattttgcttcttcatatgagtgaggaagaggcgtttaaaatgctca 2740
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Db    461 GCTTTGTACCAGGCATTTTGCGTCTTCATATGAGTGAGGAAGAGGCGTGTAAGATGCTCA 402

Qy   2741 agtttctgatgtttgacatggggctgcggaaacagtatcggccagacatgattattttac 2800
          |||||||||| |||||||||||  ||  |||| |||||||||||||||||||||||||||
Db    401 AGTTTCTGATG-TTGACATGGGCCTNNGGGNACAGNATCGGCCAGACATGATTATTTTAC 343

Qy   2801 agatccagatgtaccagctctcgaggttgcttcatgattaccacagagacctctacaatc 2860
          ||| |||||||||| |||| | | |||||||||||||||||||||||||||||||||||
Db    342 AGANCCAGATGTACCANCTCTCGGGGTTNCNTNATGATTACCACAGAGACCTCAACAATC 283

Qy   2861 acctggaggagcacgagatcggccccagcctctacgctg-ccccctggttcctcaccatg 2919
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Db    282 ACCTGGAGGAGGNCGAGATCGGCCCCAGCCTCTACGCTGCCCCCCCTGGTTCCTCACCATG 223

Qy   2920 tttgcctcacagttcccgctgggattcgtagccagagtctttgatatgatttttcttcag 2979
          |||||||||||||| |||||||||||||  ||||| |||||| ||||||||||||||||
Db    222 TTTGCCTCACAGTTGCCGCTGGGATTCGTATNCAGAGNCTTTGANATGATTTTTCTTCAG 163

Qy   2980 ggaacagaggtcatatttaaagtggctttaagtctgttgggaagccataagcccttgatt 3039
          |||||||||||||||||||||||||   ||| ||| |||||| |||||||||  |||||
Db    162 GGAACAGAGGTCATATTTAAAGTGGCGGNAAGNCTGNTGGGAANCCATAAGCCNGTGATT 103

Qy   3040 ctgcagcatgaaaacctagaaa-ccatagttgactttataaaaagcacgctacccaacct 3098
          ||||| ||||||||||||||  ||| ||| |||||||| ||||||||||||||||||||
Db    102 CTGCANCATGAAAACCTAGAANGCCAGAGTNGACTTTATGTAAAGCACGCTACCCAACCT 43

Qy   3099 tggcttggtacagatggaa-aagaccatcaatcaggtatttg 3139
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Db     42 TGGCGTGGTNNAGATGGAAGNAGACCATCAATCAGGTAGGTG 1
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RESULT   2
BM479578
LOCUS       BM479578               1051 bp    mRNA    linear   EST 05-FEB-2002
DEFINITION  AGENCOURT_6464998 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5577183
            5', mRNA sequence.
ACCESSION   BM479578
VERSION     BM479578.1  GI:18528620
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1051)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12330  row: d  column: 16
            High quality sequence stop: 662.
FEATURES             Location/Qualifiers
     source          1. .1051
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                     /note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 2.5 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
BASE COUNT      296 a    278 c    234 g    243 t
ORIGIN
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  Best Local Similarity  95.8%;  Pred. No. 1.3e-195;
  Matches  892;  Conservative    0;  Mismatches   34;  Indels    5;  Gaps    4;

Qy   2451 ccaccttaaacaccagtttcccagcaaacagcagccaaaggatgtgccatacaaagaact 2510
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CCACCTTAAACACCAGTTTCCCAGCAAACAGCAGCCAAAGGATGTGCCATACAAAGAACT 60

Qy   2511 cttaaagcagctgacttcccagcagcatgcgattcttattgaccttgggcgaacctttcc 2570
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CTTAAAGCAGCTGACTTCCCAGCAGCATGCGATTCTTATTGACCTTGGGCGAACCTTTCC 120

Qy   2571 tacacacccatacttctctgcccagcttggagcaggacagctatcgctttacaacatttt 2630
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TACACACCCATACTTCTCTGCCCAGCTTGGAGCAGGACAGCTATCGCTTTACAACATTTT 180

Qy   2631 gaaggcctactcacttctagaccaggaagtgggatattgccaaggtctcagctttgtagc 2690
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GAAGGCCTACTCACTTCTAGACCAGGAAGTGGGATATTGCCAAGGTCTCAGCTTTGTAGC 240

Qy   2691 aggcattttgcttcttcatatgagtgaggaagaggcgtttaaaatgctcaagtttctgat 2750
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Db    241 AGGCATTTTGCTTCTTCATATGAGTGAGGAAGAGGCGTTTAAAATGCTCAAGTTTCTGAT 300

Qy   2751 gtttgacatggggctgcggaaacagtatcggccagacatgattattttacagatccagat 2810
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GTTTGACATGGGGCTGCGGAAACAGTATCGGCCAGACATGATTATTTTACAGATCCAGAT 360
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Qy   2811 gtaccagctctcgaggttgcttcatgattaccacagagacctctacaatcacctggagga 2870
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Db    361 GTACCAGCTCTCGAGGTTGCTTCATGATTACCACAGAGACCTCTACAATCACCTGGAGGA 420

Qy   2871 gcacgagatcggccccagcctctacgctgccccctggttcctcaccatgtttgcctcaca 2930
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GCACGAGATCGGCCCCAGCCTCTACGCTGCCCCCTGGTTCCTCACCATGTTTGCCTCACA 480

Qy   2931 gttcccgctgggattcgtagccagagtctttgatatgatttttcttcagggaacagaggt 2990
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Db    481 GTTCCCGCTGGGATTCGTAGCCAGAGTCTTTGATATGATTTTTCTTCAGGGAACAGAGGT 540

Qy   2991 catatttaaagtggctttaagtctgttgggaagccataagcccttgattctgcagcatga 3050
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Db    541 CATATTTAAAGTGGCTTTAAGTCTGTTGGGAAGCCATAAGCCCTTGATTCTGCAGCATGA 600

Qy   3051 aaacctagaaaccatagttgactttataaaaagcacgctacccaaccttggcttggtaca 3110
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Db    601 AAACCTAGAAACCATAGTTGACTTTATAAAAAGCACGCTACCCAACCTTGGCTTGGTACA 660

Qy   3111 gatggaaaagaccatcaatcaggtatttgaaatggacatcgctaaacagttacaagctta 3170
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Db    661 GATGGAAAAGACCATCAATCAGGTATTTGAAATGGACATCGCTAAACAGTTACAAGCTTA 720

Qy   3171 tgaagttgagtaccacgtccttcaagaagaacttatcgattcctctcctctcagtgacaa 3230
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 TGAAGTTGAGTACCACGTCCTTCAAGAAGAACTTATCGATTCCTCTCCTCTCAGTGACAA 780

Qy   3231 ccaaagaatggataaattagagaaaaccaacagcagcttacgcaaacagaaccttgacct 3290
          || ||||||||||| |     ||| | |       ||||||||||||  ||||||||||
Db    781 CC-AAGAATGGATAATTAGAGAAAACCAACAGCAGGCTTACGCAAACGAAACCTTGACCC 839

Qy   3291 ccttgaacagttgcaggt-ggcaaatggtaggatccaaagccttg--aggccaccattga 3347
          | |  |||||||||||| ||| ||||||| ||||||||||| ||    | || |||| ||
Db    840 TCCTTGACAGTTGCAGGTGGGCCAATGGTAAGATCCAAAGCCCTGGAGGCCCCCCATGGA 899

Qy   3348 gaagct-cctgagcagtgagagcaagctgaa 3377
          |||||| |||||| ||| |||||||||||  ||
Db    900 AAAGCTCCCTGAACAGGGAGACCAAGCCTAA 930


RESULT   3
BM016445
LOCUS       BM016445               1007 bp    mRNA    linear   EST 30-OCT-2001
DEFINITION  603641252F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5417148 5',
            mRNA sequence.
ACCESSION   BM016445
VERSION     BM016445.1  GI:16530799
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1007)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12064  row: h  column: 13
            High quality sequence stop: 822.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /clone_lib="NIH_MGC_87"
                     /tissue_type="mammary adenocarcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 1.383 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
BASE COUNT      274 a    246 c    255 g    231 t      1 others
ORIGIN


  Query Match             23.0%;  Score 819.2;  DB 10;  Length 1007;
  Best Local Similarity   95.1%;  Pred. No. 8.9e-194;
  Matches  910;  Conservative    0;  Mismatches   39;  Indels    8;  Gaps    6;

Qy   2532 gcagcatgcgattcttattgaccttgggcgaacctttcctacacacccatacttctctgc 2591
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCAGCATGCGATTCTTATTGACCTTGGGCGAACCTTTCCTACACACCCATACTTCTCTGC 60

Qy   2592 ccagcttggagcaggacagctatcgctttacaacattttgaaggcctactcacttctaga 2651
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Db     61 CCAGCTTGGAGCAGGACAGCTATCGCTTTACAACATTTTGAAGGCCTACTCACTTCTAGA 120

Qy   2652 ccaggaagtgggatattgccaaggtctcagctttgtagcaggcattttgcttcttcatat 2711
          |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    121 CCAGGAAGTGGGATATTGCCAAGGTCTCAGCTTTGTAGCAGGCANTTTGCTTCTTCATAT 180

Qy   2712 gagtgaggaagaggcgtttaaaatgctcaagtttctgatgtttgacatggggctgcggaa 2771
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Db    181 GAGTGAGGAAGAGGCGTTTAAAATGCTCAAGTTTCTGATGTTTGACATGGGGCTGCGGAA 240

Qy   2772 acagtatcggccagacatgattatttttacagatccagatgtaccagctctcgaggttgct 2831
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACAGTATCGGCCAGACATGATTATTTTTACAGATCCAGATGTACCAGCTCTCGAGGTTGCT 300

Qy   2832 tcatgattaccacagagacctctacaatcacctggaggagcacgagatcggccccagcct 2891
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TCATGATTACCACAGAGACCTCTACAATCACCTGGAGGAGCACGAGATCGGCCCCAGCCT 360

Qy   2892 ctacgctgccccctggttcctcaccatgtttgcctcacagttcccgctgggattcgtagc 2951
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CTACGCTGCCCCCTGGTTCCTCACCATGTTTGCCTCACAGTTCCCGCTGGGATTCGTAGC 420

Qy   2952 cagagtctttgatatgatttttcttcagggaacagaggtcatatttaaagtggctttaag 3011
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Db    421 CAGAGTCTTTGATATGATTTTTCTTCAGGGAACAGAGGTCATATTTAAAGTGGCTTTAAG 480

Qy   3012 tctgttgggaagccataagcccttgattctgcagcatgaaaacctagaaaccatagttga 3071
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Db    481 TCTGTCGGGAAGCCATAAGCCCTTGATTCTGCAGCATGAAAACCTAGAAACCATAGTTGA 540

Qy   3072 ctttataaaaagcacgctacccaaccttggcttggtacagatggaaaagaccatcaatca 3131
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CTTTATAAAAAGCACGCTACCCAACCTTGGCTTGGTACAGATGGAAAAGACCATCAATCA 600

Qy   3132 ggtatttgaaatggacatcgctaaacagttacaagcttatgaagttgagtaccacgtcct 3191
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Db    601 GGTATCTGAAATGGACATCGCTAAACAGTTACAAGCTTATGAAGTTGAGTACCACGTCCT 660

Qy   3192 tcaagaagaacttatcgattcctctcctctcagtgacaaccaaagaatggataa-attag 3250
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Db    661 TCAAGAAGAACTTATCGATTCCTCTCCTCTCAGTGACAACCAAAGAATGGATAACCTTAG 720

Qy   3251 agaaaaccaacagcagcttacgcaaacagaaccttgacctccttgaacagttgca-ggtg 3309
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Db    721 AGAAAACCAACAGCAG-TTACGCAAACAGAACCTTGGACTCCTTGAACAGTTGCAGGGTG 779

Qy   3310 gcaaatggtaggatccaaagccttgaggccaccattgagaa--gctcctgagcagtgaga 3367
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Db    780 GCAAATGGTAGGATCCAAAGCCTTGAGGCCCCCATTGAGAAAGCTCCCGGAGCAGTGAGA 839

Qy   3368 gcaag--ctgaagcaggccatgcttacc-ttagaactggagcggtcggccctgctgcaga 3424
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Db    840 GCAAGGCTGGAAGCAGGCCATGCTTACCTTTAGAACTGGGAGCGGTCGGCCTGCTGCAGA 899

Qy   3425 cggtggaggagctgcggcggcggagcgcagagcccagcgaccgggagcctgagtgca 3481
          |||||||||| ||||||  | ||| |    |  ||      |||||||| |||||||
Db    900 CGGTGGAGGAACTGCGGGCGGGGAACCGCAAAGCCCAGCGACGGGAGCCGGAGTGCA 956


RESULT   4
BG828092
LOCUS       BG828092                 784 bp    mRNA    linear   EST 22-MAY-2001
DEFINITION  602753463F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4906191 5',
            mRNA sequence.
ACCESSION   BG828092
VERSION     BG828092.1  GI:14175679
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 784)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1808  row: n  column: 16
            High quality sequence stop: 784.
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                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
                     Site_2: XhoI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G).  Size-selected >500bp
                     for average insert size 1.8kb.  Library constructed by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      236 a    190 c    182 g    176 t
ORIGIN


  Query Match             22.0%;  Score 782.4;  DB 10;  Length 784;
  Best Local Similarity   99.9%;  Pred. No. 1.3e-184;
  Matches  783;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   1859 ggaaacttatgaggtatcactcagtgagcacagagacgcctcatgaacgaaaggactttg 1918
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Db      1 GGAAACTTATGAGGTATCACTCAGTGAGCACAGAGACGCCTCATGAACGAAAGGACTTTG 60

Qy   1919 aatccaaagcaaaccatcttggtgattctggtgggactcctgtgaagacccggaggcatt 1978
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Db     61 AATCCAAAGCAAACCATCTTGGTGATTCTGGTGGGACTCCTGTGAAGACCCGGAGGCATT 120

Qy   1979 cctggaggcagcagatattcctccgagtagccaccccgcagaaggcgtgcgattcttcca 2038
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Db    121 CCTGGAGGCAGCAGATATTCCTCCGAGTAGCCACCCCGCAGAAGGCGTGCGATTCTTCCA 180

Qy   2039 gcagatatgaagattattcagagctgggagagcttcccccacgatctcctttagaaccag 2098
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Db    181 GCAGATATGAAGATTATTCAGAGCTGGGAGAGCTTCCCCCACGATCTCCTTTAGAACCAG 240

Qy   2099 tttgtgaagatgggccctttggccccccaccagaggaaaagaaaaggacatctcgtgagc 2158
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Db    241 TTTGTGAAGATGGGCCCTTTGGCCCCCCACCAGAGGAAAAGAAAAGGACATCTCGTGAGC 300

Qy   2159 tccgagagctgtggcaaaaggctattcttcaacagatactgctgcttagaatggagaagg 2218
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Db    301 TCCGAGAGCTGTGGCAAAAGGCTATTCTTCAACAGATACTGCTGCTTAGAATGGAGAAGG 360

Qy   2219 aaaatcagaagctccaagcctctgaaaatgatttgctgaacaagcgcctgaagctcgatt 2278
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AAAATCAGAAGCTCCAAGCCTCTGAAAATGATTTGCTGAACAAGCGCCTGAAGCTCGATT 420

Qy   2279 atgaagaaattactccctgtcttaaagaagtaactacagtgtgggaaaagatgcttagca 2338
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Db    421 ATGAAGAAATTACTCCCTGTCTTAAAGAAGTAACTACAGTGTGGGAAAAGATGCTTAGCA 480

Qy   2339 ctccaggaagatcaaaaattaagtttgacatggaaaaaatgcactcggctgttgggcaag 2398
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Db    481 CTCCAGGAAGATCAAAAATTAAGTTTGACATGGAAAAAATGCACTCGGCTGTTGGGCAAG 540

Qy   2399 gtgtgccacgtcatcaccgaggtgaaatctggaaatttctagctgagcaattccaccttta 2458
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2459 aacaccagtttcccagcaaacagcagccaaaggatgtgccatacaaagaactcttaaagc 2518
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AACACCAGTTTCCCAGCAAACAGCAGCCAAAGGATGTGCCATACAAAGAACTCTTAAAGC 660

Qy   2519 agctgacttcccagcagcatgcgattcttattgaccttgggcgaacctttcctacacacc 2578
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    661 AGCTGACTTCCCAGCAGCATGCGATTCTTATTGACCTTGGGCGAACCTTTCCTACAAACC 720

Qy   2579 catacttctctgcccagcttggagcaggacagctatcgctttacaacattttgaaggcct 2638
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CATACTTCTCTGCCCAGCTTGGAGCAGGACAGCTATCGCTTTACAACATTTTGAAGGCCT 780

Qy   2639 actc 2642
           ||||
Db    781 ACTC 784


RESULT   5
BG759286
LOCUS       BG759286                 835 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602710975F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4851090 5',
            mRNA sequence.
ACCESSION   BG759286
VERSION     BG759286.1  GI:14069939
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 835)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1693  row: f  column: 19
            High quality sequence stop: 766.
FEATURES             Location/Qualifiers
     source          1. .835
                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:4851090"
                     /clone_lib="NIH_MGC_48"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      220 a    230 c    214 g    171 t
ORIGIN


  Query Match             20.9%;  Score 741.8;  DB 10;  Length 835;
  Best Local Similarity   98.8%;  Pred. No. 1.9e-174;
  Matches  768;  Conservative    0;  Mismatches    7;  Indels    2;  Gaps    2;

Qy   1591 gatagctccctgtctagtacattaagtaacaccagcaaagagccatctgtgtgtgaaaag 1650
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GATAGCTCCCTGTCTAGTACATTAAGTAACACCAGCAAAGAGCCATCTGTGTGTGAAAAG 60

Qy   1651 gaggccttgcccatctctgagagctcctttaagctcctcggctcctcggaggacctgtcc 1710
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GAGGCCTTGCCCATCTCTGAGAGCTCCTTTAAGCTCCTCGGCTCCTCGGAGGACCTGTCC 120

Qy   1711 agtgactcggagagtcatctcccagaagagccagctccgctgtcgccccagcaggccttc 1770
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGTGACTCGGAGAGTCATCTCCCAGAAGAGCCAGCTCCGCTGTCGCCCCAGCAGGCCTTC 180

Qy   1771 aggaggcgagcaaacaccctgagtcacttccccatcgaatgccaggaacctccacaacct 1830
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AGGAGGCGAGCAAACACCCTGAGTCACTTCCCCATCGAATGCCAGGAACCTCCACAACCT 240

Qy   1831 gcccgggggtccccgggggtttcgcaaaggaaacttatgaggtatcactcagtgagcaca 1890
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GCCCGGGGGTCCCCGGGGGTTTCGCAAAGGAAACTTATGAGGTATCACTCAGTGAGCACA 300

Qy   1891 gagacgcctcatgaacgaaaggactttgaatccaaagcaaaccatcttggtgattctggt 1950
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GAGACGCCTCATGAACGAAAGGACTTTGAATCCAAAGCAAACCATCTTGGTGATTCTGGT 360

Qy   1951 gggactcctgtgaagacccggaggcattcctggaggcagcagatattcctccgagtagcc 2010
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Db    361 GGGACTCCTGTGAAGACCCGGAGGCATTCCTGGAGGCAGCAGATATTCCTCCGAGTAGCC 420

Qy   2011 accccgcagaaggcgtgcgattcttccagcagatatgaagattattcagagctgggagag 2070
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ACCCCGCAGAAGGCGTGCGATTCTTCCAGCAGATATGAAGATTATTCAGAGCTGGGAGAG 480

Qy   2071 cttcccccacgatctcctttagaaccagtttgtgaagatgggcccttggccccccacca 2130
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CTTCCCCCACGATCTCCTTTAGAACCAGTTTGTGAAGATGGGCCCTTTGGCCCCCCACCA 540

Qy   2131 gaggaaaagaaaaggacatctcgtgagctccgagagctgtggcaaaaggctattcttcaa 2190
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAGGAAAAGAAAAGGACATCTCGTGAGCTCCGAGAGCTGTGGCAAAAGGCTATTCTTCAA 600

Qy   2191 cagatactgctgcttagaatggagaaggaaaatcagaagctccaagcctctgaaaatgat 2250
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CAGATACTGCTGCTTAGAATGGAGAAGGAAAATCAGAAGCTCCAAGCCTCTGAACATGAT 660

Qy   2251 ttgctgaacaagcgcctgaagctcgattatgaagaaattactccctgtcttaaagaagta 2310
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TTGCTGAACAAGCGCCTGAAGCTCGATTATGACGAAATTACTCCCTGTCTTAAAGAAGTA 720

Qy   2311 actacagtgt-gggaaaagatgctta-gcactccaggaagatcaaaaattaagtttg 2365
           |||||||||| ||||| |||||||| |||||||||||||||||| ||| | ||| |
Db    721 ACTACAGTGTGGGGAACAGATGCTTAGGCACTCCAGGAAGATCAACAATCAGGTTCG 777
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RESULT   6
BG746377
LOCUS       BG746377                 800 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602703644F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4856891 5',
            mRNA sequence.
ACCESSION   BG746377
VERSION     BG746377.1  GI:14057030
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 800)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: NIH Intramural Sequencing Center
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1708  row: h  column: 12
            High quality sequence stop: 762.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:4856891"
                     /clone_lib="NIH_MGC_15"
                     /tissue_type="adenocarcinoma cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)"
BASE COUNT      213 a    218 c    203 g    166 t
ORIGIN


  Query Match             20.8%;  Score 738.8;  DB 10;  Length 800;
  Best Local Similarity   98.6%;  Pred. No. 1.1e-173;
  Matches  787;  Conservative    0;  Mismatches    7;  Indels    4;  Gaps    4;

Qy   1502 agagatctttaacagagtctttagaaagtattttgtcccggggtaataaagccagaggcc 1561
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 AGAGATCTTTAACAGAGTCTTTAGAAAGTATTTTGTCCCGGGGTAATAAAGCCAGAGGCC 61

Qy   1562 tgcaggaacactccatcagtgtggatctggatagctccctgtctagtacattaagtaaca 1621
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 TGCAGGAACACTCCATCAGTGTGGATCTGGATAGCTCCCTGTCTAGTACATTAAGTAACA 121

Qy   1622 ccagcaaagagccatctgtgtgtgaaaaggaggccttgcccatctctgagagctccttta 1681
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    122 CCAGCAAAGAGCCATCTGTGTGTGAAAAGGAGGCCTTGCCCATCTCTGAGAGCTCCTTTA 181

Qy   1682 agctcctcggctcctcggaggacctgtccagtgactcggagagtcatctcccagaagagc 1741
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    182 AGCTCCTCGGCTCCTCGGAGGACCTGTCCAGTGACTCGGAGAGTCATCTCCCAGAAGAGC 241

Qy   1742 cagctccgctgtcgccccagcaggccttcaggaggcgagcaaacaccctgagtcacttcc 1801
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    242 CAGCTCCGCTGTCGCCCCAGCAGGCCTTCAGGAGGCGAGCAAACACCCTGAGTCACTTCC 301
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Qy   1802 ccatcgaatgccaggaacctccacaacctgcccgggggtccccgggggtttcgcaaagga 1861
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    302 CCATCGAATGCCAGGAACCTCCACAACCTGCCCGGGGGTCCCCGGGGGTTTCGCAAAGGA 361

Qy   1862 aacttatgaggtatcactcagtgagcacagagacgcctcatgaacgaaaggactttgaat 1921
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    362 AACTTATGAGGTATCACTCAGTGAGCACAGAGACGCCTCATGAACGAAAGGACTTTGAAT 421

Qy   1922 ccaaagcaaaccatcttggtgattctggtgggactcctgtgaagacccggaggcattcct 1981
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    422 CCAAAGCAAACCATCTTGGTGATTCTGGTGGGACTCCTGTGAAGACCCGGAGGCATTCCT 481

Qy   1982 ggaggcagcagatattcctccgagtagccaccccgcagaaggcgtgcgattcttccagca 2041
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    482 GGAGGCAGCAGATATTCCTCCGAGTAGCCACCCCGCAGAAGGCGTGCGATTCTTCCAGCA 541

Qy   2042 g-atatgaagattattcagagctgggagagcttcccccacgatctcctttagaaccagtt 2100
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    542 GCATATGAAGATTATTCAGAGCTGGGAGAGCTTCCCCCACGATCTCCTTTAGAACCAGTT 601

Qy   2101 tgtgaa-gatgggccctttggccccccaccagaggaaaagaaaaggacatctcgtgagct 2159
          |||||| ||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db    602 TGTGAACGATGGGCCCTTTGGCCCCCCACCAGAGGAACAGAAAAGGACATCTCGTGAGCT 661

Qy   2160 ccgagagctgtggcaaaaggctattcttcaacagatactgctgcttagaatgga-gaagg 2218
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db    662 CCGAGAGCTGTGGCAAAAGGCTATTCTTCAACAGATACTGCTGCTTAGAATGGACGAAGG 721

Qy   2219 aaaatcagaagctccaagcctctgaaaatgatttgctg-aacaagcgcctgaagctcgat 2277
          |||||||||||||||| |||||| |||||||||||| ||| ||||||||||||||||||
Db    722 CAAATCAGAAGCTCCAAGCTTCTGAACATGATTTGCTGAAACCAGCGCCTGAAGCTCGAT 781

Qy   2278 tatgaagaaattactccc 2295
          |||||||||| ||||||
Db    782 CATGAAGAAATCACTCCC 799
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RESULT   7
BM476629
LOCUS       BM476629                1121 bp    mRNA    linear   EST 05-FEB-2002
DEFINITION  AGENCOURT_6476337 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:5553589
            5', mRNA sequence.
ACCESSION   BM476629
VERSION     BM476629.1  GI:18525671
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1121)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12270  row: m  column: 14
            High quality sequence start: 6
            High quality sequence stop: 636.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /clone_lib="NIH_MGC_85"
                     /tissue_type="lymphoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lymph; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 1.867 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
BASE COUNT      312 a    277 c    280 g    251 t      1 others
ORIGIN
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  Best Local Similarity   96.1%;  Pred. No. 2.8e-173;
  Matches  799;  Conservative    0;  Mismatches   26;  Indels    6;  Gaps    4;

Qy    830 acaatattgtgcagcccacagatatcgaggaaaatcgaactatgctcttcacgattggcc 889
          || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     31 ACTATATTGTGCAGCCCACAGATATCGAGGAAAATCGAACTATGCTCTTCACGATTGGCC 90

Qy    890 agtctgaagtttacctcatcagtcctgacaccaaaaaaaatagcat-tggagaaaaatttt 948
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db     91 AGTCTGAAGTTTACCTCATCAGTCCTGACACCAAAAAAATAGCATNTGGAGAAAAATTTT 150

Qy    949 aaggagatatccttttgctctcagggcatcagacacgtggaccactttgggtttatctgt 1008
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    151 AAGGAGATATCCTTTTGCTCTCAGGGCATCAGACACGTGGACCACTTTGGGTTTATCTGT 210

Qy   1009 cgggagtcttccggaggtggcggctttcattttgtctgttacgtgtttcagtgcacaaat 1068
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    211 CGGGAGTCTTCCGGAGGTGGCGGCTTTCATTTTGTCTGTTACGTGTTTCAGTGCACAAAT 270

Qy   1069 gaggctctggttgatgaaattatgatgaccctgaaacaggccttcacggtggccgcagtg 1128
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    271 GAGGCTCTGGTTGATGAAATTATGATGACCCTGAAACAGGCCTTCACGGTGGCCGCAGTG 330

Qy   1129 cagcagacagctaaggcgccagcccagctgtgtgagggctgccccctgcaaagcctgcac 1188
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    331 CAGCAGACAGCTAAGGCGCCAGCCCAGCTGTGTGAGGGCTGCCCCCTGCAAAGCCTGCAC 390

Qy   1189 aagctctgtgagaggatagagggaatgaattcttccaaaacaaaactagaactgcaaaag 1248
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    391 AAGCTCTGTGAGAGGATAGAGGGAATGAATTCTTCCAAAACAAAACTAGAACTGCAAAAG 450

Qy   1249 cacctgacgacattaaccaatcaggagcaggcgactatttttgaagaggttcagaaattg 1308
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    451 CACCTGACGACATTAACCAATCAGGAGCAGGCGACTATTTTTGAAGAGGTTCAGAAATTG 510

Qy   1309 agaccgagaaatgagcagcgagagaatgaattgattatttctttttctgagatgtttatat 1368
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    511 AGACCGAGAAATGAGCAGCGAGAGAATGAATTGATTATTTCTTTTCTGAGATGTTTATAT 570

Qy   1369 gaagagaaacagaaagaacacatccatattggggagatgaagcagacatcgcagatggca 1428
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    571 GAAGAGAAACAGAAAGAACACATCCATATTGGGGAGATGAAGCAGACATCGCAGATGGCA 630

Qy   1429 gcagagaatattggaagtgaattaccacccagtgccactcgatttaggctagatatgctg 1488
          |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db    631 GCAGAGAATATTGGAAGTGAATTACCACCCAGTGCCCCTCGATTTAGGCTAGATATGCTG 690

Qy   1489 aaaaacaaagcaaagagatctttaacagagtctttagaaagtattttgtcccggggtaat 1548
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    691 AAAAACAAAGCAAAGAGATCTTTAACAGAGTCTTTAGAAAGTATTTTGTCCCGGGGTAAT 750

Qy   1549 aaagccagaggcctgcaggaacactccatcagtgt---ggatctggatagctcccct-gtc 1604
          |||||||||||||||||| |  | |      ||   |||||||||||||||||| |||
Db    751 AAAGCCAGAGGCCTGCAGGGAACCCTCCATCCCGTGTGGGATCTGGATAGCTCCCTGGTC 810

Qy   1605 tagtaca-ttaagtaacaccagcaaagagccatctgtgtgtgaaaaggagg 1654
          ||||||| ||||||||||||||||||     |      |||||| |||   ||
Db    811 TAGTACATTTAAGTAACACCAGCAAAAGAGCCATCCTGTGTGTAAAAAGGG 861
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RESULT   8
BM460573
LOCUS       BM460573                1109 bp    mRNA    linear   EST 05-FEB-2002
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DEFINITION  AGENCOURT_6421241 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5531908
            5', mRNA sequence.
ACCESSION   BM460573
VERSION     BM460573.1  GI:18509613
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1109)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12214  row: f  column: 05
            High quality sequence stop: 630.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:5531908"
                     /clone_lib="NIH_MGC_71"
                     /tissue_type="leiomyosarcoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 2.1 kb.  "
BASE COUNT      301 a    311 c    258 g    239 t
ORIGIN
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  Best Local Similarity   97.5%;  Pred. No. 2.2e-171;
  Matches  773;  Conservative    0;  Mismatches   17;  Indels    3;  Gaps    3;

Qy   1340 tgattatttcttttctgagatgtttatatgaagagaaacagaaagaacacatccatattg 1399
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     13 TGATTATTTCTTTTCTGAGATGTTTATATGAAGAGAAACAGAAAGAACACATCCATATTG 72

Qy   1400 gggagatgaagcagacatcgcagatggcagcagagaatattggaagtgaattaccaccca 1459
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     73 GGGAGATGAAGCAGACATCGCAGATGGCAGCAGAGAATATTGGAAGTGAATTACCACCCA 132

Qy   1460 gtgccactcgatttaggctagatatgctgaaaaacaaagcaaagagatctttaacagagt 1519
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    133 GTGCCACTCGATTTAGGCTAGATATGCTGAAAAACAAAGCAAAGAGATCTTTAACAGAGT 192

Qy   1520 ctttagaaagtattttgtcccggggtaataaagccagaggcctgcaggaacactccatca 1579
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    193 CTTTAGAAAGTATTTTGTCCCGGGGTAATAAAGCCAGAGGCCTGCAGGAACACTCCATCA 252

Qy   1580 gtgtggatctggatagctccctgtctagtacattaagtaacaccagcaaagagccatctg 1639
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    253 GTGTGGATCTGGATAGCTCCCTGTCTAGTACATTAAGTAACACCAGCAAAGAGCCATCTG 312

Qy   1640 tgtgtgaaaaggaggccttgcccatctctgagagctcctttaagctcctcggctcctcgg 1699
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    313 TGTGTGAAAAGGAGGCCTTGCCCATCTCTGAGAGCTCCTTTAAGCTCCTCGGCTCCTCGG 372

Qy   1700 aggacctgtccagtgactcggagagtcatctcccagaagagccagctccgctgtcgcccc 1759
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    373 AGGACCTGTCCAGTGACTCGGAGAGTCATCTCCCAGAAGAGCCAGCTCCGCTGTCGCCCC 432

Qy   1760 agcaggccttcaggaggcgagcaaacaccctgagtcacttccccatcgaatgccaggaac 1819
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    433 AGCAGGCCTTCAGGAGGCGAGCAAACACCCTGAGTCACTTCCCCATCGAATGCCAGGAAC 492

Qy   1820 ctccacaacctgcccgggggtccccgggggtttcgcaaaggaaacttatgaggtatcact 1879
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    493 CTCCACAACCTGCCCGGGGGTCCCCGGGGGTTTCGCAAAGGAAACTTATGAGGTATCACT 552

Qy   1880 cagtgagcacagagacgcctcatgaacgaaaggactttgaatccaaagcaaaccatcttg 1939
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    553 CAGTGAGCACAGAGACGCCTCATGAACGAAAGGACTTTGAATCCAAAGCAAACCATCTTG 612

Qy   1940 gtgattctggtgggactcctgtgaagacccggaggcattcctggaggcagcagatattcc 1999
          ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db    613 GTGATTCTGGTGGGACTCCTGTGAAGACCCCGGAGCATTCCTGGAGGCAGCAGATATTCC 672

Qy   2000 tccgagtagccaccccgcagaaggcgtgcgattcttccagcagatatgaagattattcag 2059
          ||||||||||||||||||||||||||| ||||||||||||||||||||| |||||||| |
Db    673 TCCGAGTAGCCACCCCGCAGAAGGCGGGCGATTCTTCCAGCAGATATGGAGATTATTCCG 732

Qy   2060 agct-gggagagcttcccccacgatc-tcctttagaaccagtttgt-gaagatgggccct 2116
          |||| |||||||||||||| | | | ||| |||||||||||||| ||||||||| ||
Db    733 AGCTGGGGAGAGCTTCCCCCCCCAACTTCCCTTAGAACCAGTTTGTGGAAGATGGGGCCC 792

Qy   2117 ttggccccccacc 2129
          || |  | || ||
Db    793 TTTGGGCGCCTCC 805
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RESULT   9
BE299948
LOCUS       BE299948                952 bp    mRNA    linear   EST 20-JUL-2000
DEFINITION  600944494F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960782 5',
            mRNA sequence.
ACCESSION   BE299948
VERSION     BE299948.1  GI:9183696
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 952)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM54  row: k  column: 23
            High quality sequence stop: 709.
FEATURES             Location/Qualifiers
     source          1. .952
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                     /db_xref="taxon:9606"
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                     /clone_lib="NIH_MGC_17"
                     /tissue_type="rhabdomyosarcoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
                     Site_2: XhoI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G).  Size-selected >500bp
                     for average insert size 1.8kb.  Library constructed by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      249 a    240 c    250 g    212 t      1 others
ORIGIN
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  Query Match           20.3%;  Score 722.2;  DB 10;  Length 952;
  Best Local Similarity  97.2%;  Pred. No. 1.7e-169;
  Matches  766;  Conservative    0;  Mismatches   19;  Indels    3;  Gaps    3;

Qy   1879 tcagtgagcacagagacgcctcatgaacgaaaggactttgaatccaaagcaaaccatctt 1938
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TCAGTGAGCACAGAGACGCCTCATGAACGAAAGGACTTTGAATCCAAAGCAAACCATCTT 60

Qy   1939 ggtgattctggtgggactcctgtgaagacccggaggcattcctggaggcagcagatattc 1998
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GGTGATTCTGGTGGGACTCCTGTGAAGACCCGGAGGCATTCCTGGAGGCAGCAGATATTC 120

Qy   1999 ctccgagtagccaccccgcagaaggcgtgcgattcttccagcagatatgaagattattca 2058
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CTCCGAGTAGCCACCCCGCAGAAGGCGTGCGATTCTTCCAGCAGATATGAAGATTATTCA 180

Qy   2059 gagctgggagagcttcccccacgatctcctttagaaccagtttgtgaagatgggcccttt 2118
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GAGCTGGGAGAGCTTCCCCCACGATCTCCTTTAGAACCAGTTTGTGAAGATGGGCCCTTT 240

Qy   2119 ggcccccccaccagaggaaaagaaaaggacatctcgtgagctccgagagctgtggcaaaag 2178
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GGCCCCCCACCAGAGGAAAAGAAAAGGACATCTCGTGAGCTCCGAGAGCTGTGGCAAAAG 300

Qy   2179 gctattcttcaacagatactgctgcttagaatggagaaggaaaatcagaagctccaagcc 2238
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GCTATTCTTCAACAGATACTGCTGCTTAGAATGGAGAAGGAAAATCAGAAGCTCCAAGCC 360

Qy   2239 tctgaaaatgatttgctgaacaagcgcctgaagctcgattatgaagaaattactccctgt 2298
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TCTGAAAATGATTTGCTGAACAAGCGCCTGAAGCTCGATTATGAAGAAATTACTCCCTGT 420

Qy   2299 cttaaagaagtaactacagtgtgggaaaagatgcttagcactccaggaagatcaaaaatt 2358
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CTTAAAGAAGTAACTACAGTGTGGGAAAAGATGCTTAGCACTCCAGGAAGATCAAAAATT 480

Qy   2359 aagtttgacatggaaaaaatgcactcggctgttgggcaaggtgtgccacgtcatcaccga 2418
          |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db    481 AAGTTTGACATGGAAAAAATGCACTCGGCTG-TGGGCAAGGTGTGCCACGTCATCACCGA 539

Qy   2419 ggtgaaatctggaaatttctagctgagcaattccaccttaaacaccagtttcccagcaaa 2478
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    540 GGTGAAATCTGGAAATTTCTAGCTGAGCAATTCCACCTTAAACACCAGTTTCCCAGCAAA 599

Qy   2479 cagcagccaaaggatgtgccatacaaagaactcttaaagcagctgacttcccagcagcat 2538
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    600 CAGCAGCCAAAGGATGTGCCATACAAAGAACTCTTAAAGCAGCTGACTTCCCAGCAGCAT 659

Qy   2539 gcgattctta-ttgaccttgggcgaacctttcctacacacccatacttctctgcccagct 2597
          |||||||||| ||||||| ||||||||||||||||||||||||||||||||||||| | |
Db    660 GCGATTCTTATTTGACCTGNGGCGAACCTTTCCTACACACCCATACTTCTCTGCCCAG-T 718

Qy   2598 tggagcaggacagctatcgctttacaacattttgaaggcctactcacttctagaccagga 2657
          |||||||||||||||||||||||||||||||   ||| ||||||   |      |||||
Db    719 TGGAGCAGGACAGCTATCGCTTTACAACATTTGTGAGGGCTACTCCACTTCTAGACAGGA 778

Qy   2658 agtgggat 2665
          || ||
Db    779 GTGGGTAT 786


RESULT  10
BI907513
LOCUS       BI907513                838 bp    mRNA    linear   EST 16-OCT-2001
DEFINITION  603065640F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5214945 5',
            mRNA sequence.
ACCESSION   BI907513
VERSION     BI907513.1  GI:16170347
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 838)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11539  row: o  column: 10
            High quality sequence start: 4
            High quality sequence stop: 780.
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                     /clone="IMAGE:5214945"
                     /clone_lib="NIH_MGC_118"
                     /tissue_type="leukocyte"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
                     (destroyed); RNA source leukocytes from anonymous pool of
                     non-activated  adult donors.  Library is oligo-dT primed
                     and directionally cloned  (EcoRV site is destroyed upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     1.2-3.3 kb.  Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen).  Research Genetics tracking code 027. Note:
                     this is a NIH_MGC Library."
BASE COUNT      237 a    199 c    191 g    211 t
ORIGIN


  Query Match           20.1%;  Score 713.8;  DB 10;  Length 838;
  Best Local Similarity  97.0%;  Pred. No. 2e-167;
  Matches  812;  Conservative    0;  Mismatches   17;  Indels    8;  Gaps    8;

Qy   2226 gaagctccaagcctctgaaaatgatttgctgaacaagcgcctgaagctcgattatgaaga 2285
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      9 GAAGCTCCAAGCCTCTGAAAATGATTTGCTGAACAAGCGCCTGAAGCTCGATTATGAAGA 68

Qy   2286 aattactccctgtcttaaagaagtaactacagtgtgggaaaagatgcttagcactccagg 2345
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     69 AATTACTCCCTGTCTTAAAGAAGTAACTACAGTGTGGGAAAAGATGCTTAGCACTCCAGG 128

Qy   2346 aagatcaaaaattaagtttgacatggaaaaaatgcactcggctgttgggcaaggtgtgcc 2405
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    129 AAGATCAAAAATTAAGTTTGACATGGAAAAAATGCACTCGGCTGTTGGGCAAGGTGTGCC 188

Qy   2406 acgtcatcaccgaggtgaaatctggaaatttctagctgagcaattccaccttaaacacca 2465
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    189 ACGTCATCACCGAGGTGAAATCTGGAAATTTCTAGCTGAGCAATTCCACCTTAAACACCA 248

Qy   2466 gtttcccagcaaacagcagccaaaggatgtgccatacaaagaactcttaaagcagctgac 2525
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Db    249 GTTTCCCAGCAAACAGCAGCCAAAGGATGTGCCATACAAAGAACTCTTAAAGCAGCTGAC 308

Qy   2526 ttcccagcagcatgcgattcttattgaccttgggcgaacctttcctacacacccatactt 2585
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db    309 TTCCCAGCAGCATGCGATTCTTA-TGACCTTGGGCGAACCTTTCCTACACACCCATACTT 367

Qy   2586 ctctgcccagcttggagcaggacagctatcgctttacaacattttgaaggcctactcact 2645
          |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db    368 CTCTGCCCAGCTTGGAGCAGGACAGCTATCGCTTTACAACA-TTTGAAGGCCTACTCACT 426

Qy   2646 tctagaccaggaagtgggatattgccaaggtctcagctttgtagcaggcattttgcttct 2705
          |||||||||||||||||||| |||||||||||||||| |||||||||| |||||||||
Db    427 TCTAGACCAGGAAGTGGGATA-TGCCAAGGTCTCAGC-TTGTAGCAGGCA-TTTGCTTCT 483
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Qy   2706 tcatatgagtgaggaagaggcgtttaaaatgctcaagtttctgatgtttgacatggggct 2765
          ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    484 TCATATGAGTGAGGAAGAGGCGTTTAAAATGCTCAAGTTTCTGATG-TTGACATGGGGCT 542

Qy   2766 gcggaaacagtatcggccagacatgattattttacagatccagatgtaccagctctcgag 2825
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    543 GCGGAAACAGTATCGGCCAGACATGATTATTTTACAGATCCAGATGTACCAGCTCTCGAG 602

Qy   2826 gttgcttcatgattaccacagagacctctacaatcacctggaggagcacgagatcggccc 2885
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    603 GTTGCTTCATGATTACCACAGAGACCTCTACAATCACCTGGAGGAGCACGAGATCGGCCC 662

Qy   2886 cagcctctacgctg-ccccctggttcctcaccatgtttgcctcacagttcccgctgggat 2944
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    663 CAGCCTCTACGCTGCCCCCCTGGTTCCTCACCATGTTTGCCTCACAGTTCCCGCTGGGAT 722

Qy   2945 tcgtagccagagtctttgatatgatttttcttcagggaacagaggtcatatttaaagtgg 3004
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    723 TCGTAGCCAGAGTCTTTGATATGATTTTTCTTCAGGGAACAGAGGTCATATTTAAAGTGG 782

Qy   3005 ctttaagtctgttgggaagccataagcccttgattctgcagcatgaaaacctagaaa 3061
          |||||  ||   ||||||| |||||||||  |        ||||||||||||||
Db    783 -TTTAAATCCTGTGGGAAGGCATAAGCCCTGATTCTGCAGCATTGAAAACCTAGAAA 838


RESULT  11
BG120498
LOCUS       BG120498                807 bp    mRNA    linear   EST 30-JAN-2001
DEFINITION  602346815F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4441923 5',
            mRNA sequence.
ACCESSION   BG120498
VERSION     BG120498.1  GI:12614007
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 807)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10213  row: n  column: 04
            High quality sequence stop: 682.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /clone_lib="NIH_MGC_90"
                     /tissue_type="adenocarcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 1.7 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
BASE COUNT      231 a    197 c    189 g    190 t
ORIGIN


  Query Match           19.8%;  Score 705;  DB 10;  Length 807;
  Best Local Similarity   96.1%;  Pred. No. 3.1e-165;
  Matches  766;  Conservative    0;  Mismatches   25;  Indels    6;  Gaps    4;

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Db      1 GATATTCCTCCGAGTAGCCACCCCGCAGAAGGCGTGCGATTCTTCCAGCAGATATGAAGA 60

Qy   2052 ttattcagagctgggagagcttcccccacgatctcctttagaaccagtttgtgaagatgg 2111
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TTATTCAGAGCTGGGAGAGCTTCCCCCACGATCTCCTTTAGAACCAGTTTGTGAAGATGG 120

Qy   2112 gccctttggccccccaccagaggaaaagaaaaggacatctcgtgagctccgagagctgtg 2171
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GCCCTTTGGCCCCCCACCAGAGGAAAAGAAAAGGACATCTCGTGAGCTCCGAGAGCTGTG 180

Qy   2172 gcaaaaggctattcttcaacagatactgctgcttagaatggagaaggaaaatcagaagct 2231
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GCAAAAGGCTATTCTTCAACAGATACTGCTGCTTAGAATGGAGAAGGAAAATCAGAAGCT 240

Qy   2232 ccaagcctctgaaaatgatttgctgaacaagcgcctgaagctcgattatgaagaaattac 2291
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CCAAGCCTCTGAAAATGATTTGCTGAACAAGCGCCTGAAGCTCGATTATGAAGAAATTAC 300

Qy   2292 tccctgtcttaaagaagtaactacagtgtgggaaaagatgcttagcactccaggaagatc 2351
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Db    301 TCCCTGTCTTAAAGAAGTAACTACAGTGTGGGAAAAGATGCTTAGCACTCCAGGAAGATC 360

Qy   2352 aaaaattaagtttgacatggaaaaaatgcactcggctgttgggcaaggtgtgccacgtca 2411
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Db    361 AAAAATTAAGTTTGACATGGAAAAAATGCACTCGGCTGTTGGGCAAGGTGTGCCACGTCA 420

Qy   2412 tcaccgaggtgaaatctggaaatttctagctgagcaattccaccttaaacaccagtttcc 2471
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TCACCGAGGTGAAATCTGGAAATTTCTAGCTGAGCAATTCCACCTTAAACACCAGTTTCC 480

Qy   2472 cagcaaacagcagccaaaggatgtgccatacaaagaactcttaaagcagctgacttccca 2531
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CAGCAAACAGCAGCCAAAGGATGTGCCATACAAAGAACTCTTAAAGCAGCTGACTTCCCA 540

Qy   2532 gcagcatgcgattcttattgaccttgggcgaacctttcctacaca-cccatacttctctg 2590
          |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db    541 GCAGCATGCGATTCTTATTGACCTTGGGCGAACCTTTCCTACACAGCCCATACTTCTCTG 600

Qy   2591 cccagcttggagcaggacagctatcgctttacaacattttgaaggcctactcacttctag 2650
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2651 accaggaagtgggatattgcc--aaggtctcagcttt-gtagcaggcattttgcttcttc 2707
          |||||||||||||||||||  |||   |||||||| || |||||| | |||||||  ||
Db    661 ACCAGGAAGTGGGATATTGCCCAAAGTCTTCAGCTTTGGTGGCAGGCCTCTTGCTTCCTC 720

Qy   2708 atatgagtgaggaagaggcgtttaaaatgctcaagtttctgatgtttgacatggggctgc 2767
          |||||||||| |||||||||||  |||     ||   ||| ||||||||||||||| |
Db    721 ATATGAGTGACGAAGAGGCGTTAAAATGCTCCA--GTTCCGATGTTTGACATGGGCCGCG 778

Qy   2768 ggaaacagtatcggcca 2784
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Db    779 GGAACCAGTTCGGGCAA 795


RESULT  12
BM014940
LOCUS       BM014940                832 bp    mRNA    linear   EST 30-OCT-2001
DEFINITION  603640877F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5416818 5',
            mRNA sequence.
ACCESSION   BM014940
VERSION     BM014940.1  GI:16529294
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 832)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
```

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COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12063  row: j  column: 19
            High quality sequence stop: 811.
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                    /note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI;
                    Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                    Average insert size 1.383 kb. Library enriched for
                    full-length clones and constructed by Life Technologies.
                    Note: this is a NIH_MGC Library."
BASE COUNT      231 a    205 c    186 g    208 t      2 others
ORIGIN


  Query Match             19.7%;  Score 701;  DB 10;  Length 832;
  Best Local Similarity   97.5%;  Pred. No. 3.1e-164;
  Matches  785;  Conservative    0;  Mismatches   12;  Indels    8;  Gaps    7;

Qy    2405 cacgtcatcaccgaggtgaaatctggaaatttctagctgagcaattccaccttaaacacc 2464
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      29 CACGTCATCACCGAGGTGAAATCTGGAAATTTCTAGCTGAGCAATTCCACCTTAAACACC 88

Qy    2465 agtttcccagcaaacagcagccaaaggatgtgccatacaaagaactcttaaagcagctga 2524
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      89 AGTTTCCCAGCAAACAGCAGCCAAAGGATGTGCCATACAAAGAACTCTTAAAGCAGCTGA 148

Qy    2525 cttcccagcagcatgcgattcttattgaccttgggcgaacctttcctacacacccatact 2584
           |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db     149 CTTCCCAGCAGCATGCGATTCTTA-TGACCTTGGGCGAACCTTTCCTACACACCCATACT 207

Qy    2585 tctctgcccagcttggagcaggacagctatcgctttacaacattttgaaggcctactcac 2644
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     208 TCTCTGCCCAGCTTGGAGCAGGACAGCTATCGCTTTACAACATTTTGAAGGCCTACTCAC 267

Qy    2645 ttctagaccaggaagtgggatattgccaaggtctcagctttgtagcaggcattttgcttc 2704
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db     268 TTCTAGACCAGGAAGTGGGATATTGCCAAGGTCTCAGCTTTGTAGCAGGCATTNTGCTTC 327

Qy    2705 ttcatatgagtgaggaagaggcgtttaaaatgctcaagtttctgatgtttgacatggggc 2764
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     328 TTCATATGAGTGAGGAAGAGGCGTTTAAAATGCTCAAGTTTCTGATGTTTGACATGGGGC 387

Qy    2765 tgcggaaacagtatcggccagacatgattattttacagatccagatgtaccagctctcga 2824
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     388 TGCGGAAACAGTATCGGCCAGACATGATTATTTTACAGATCCAGATGTACCAGCTCTCGA 447

Qy    2825 ggttgcttcatgattaccacagagacctctacaatcacctggaggagcacgagatcggcc 2884
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     448 GGTTGCTTCATGATTACCACAGAGACCTCTACAATCACCTGGAGGAGCACGAGATCGGCC 507

Qy    2885 ccagcctctacgctgccccctggttcctcaccatgtttgcctcacagttcccgctgggat 2944
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     508 CCAGCCTCTACGCTGCCCCCTGGTTCCTCACCATGTTTGCCTCACAGTTCCCGCTGGGAT 567

Qy    2945 tcgtagccagagtctttgatatgatttttcttcagggaacagaggtcatatttaa-agtg 3003
           |||||||||||||||||||||||||||||||||||||||||||||||||||| |||| |||
Db     568 TCGTAGCCAGAGTCTTTGATATGATTTTTCTTCAGGGAACAGAGGTCATATTTAACAGTG 627

Qy    3004 gctttaagtctgttgggaagccataagcccttgattctgcagcatgaaaacctagaaacc 3063
           |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db     628 GCTTTAAGTCTGNTGGGAAGCCATAAGCCCTTGATTCTGCAGCATGAAAACCTAGAAACC 687

Qy    3064 atagttgacttttat-aaaaagcacgctacccaaccttggc-ttggtacagat-ggaaaag 3120
           |||||||||||||| |||||||||||||| |||| |||||| |||||||||| |||||||
Db     688 ATAGTTGACTTTATAAAAAAGCACGCTAACCAAGCTTGGCTTTGGTACAGATGGGAAAAG 747

Qy    3121 accatcaatcaggtatttgaaatggacatcgctaaa--cagttacaagcttatgaagttg 3178
           |||||||||||||||||| |||||||||||| ||||     |   ||||||||||||||||
Db     748 ACCATCAATCAGGTATTGGAAATGGACATCGGTAAAACAGTTACAAAGCTTATGAAGTTG 807

Qy    3179 agtacc-acgtccttcaagaagaac 3202
           |||||| ||||||||||||||||||
Db     808 AGTACCAACGTCCTTCAAGAAGAAC 832


RESULT  13
AL570425
LOCUS       AL570425                851 bp    mRNA    linear   EST 16-FEB-2001
DEFINITION  AL570425 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI020YF02 5
            prime, mRNA sequence.
ACCESSION   AL570425
VERSION     AL570425.1  GI:12926720
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 851)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES            Location/Qualifiers
     source         1. .851
                    /organism="Homo sapiens"
                    /db_xref="taxon:9606"
                    /clone="CS0DI020YF02"
                    /clone_lib="LTI_NFL006_PL2"
                    /tissue_type="placenta"
                    /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                    was primed with a NotI-oligo(dT) primer.  Five prime end
                    enriched, double-stranded cDNA was digested with Not I and
                    cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                    vector. Library was normalized. Library was constructed by
                    Life Technologies. Contact : Feng Liang Life Technologies,
                    a division of Invitrogen 9800 Medical Center Drive
                    Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                    Email : fliang@lifetech.com URL :
                    http://fulllength.invitrogen.com"
BASE COUNT      240 a    214 c    220 g    174 t      3 others
ORIGIN


  Query Match             19.4%;  Score 689.8;  DB 9;  Length 851;
  Best Local Similarity   98.9%;  Pred. No. 2e-161;
  Matches  714;  Conservative    1;  Mismatches    4;  Indels    3;  Gaps    2;

Qy    2836 gattaccacagagacctctacaat--cacctggaggagcacgagatcggccccagcctct 2893
           |||||||||||||||||||||||     | ||||||||||||||||||||||||||||||
Db       1 GATTACCACAGAGACCTCTACAANTCACCTTGGAGGAGCACGAGATCGGCCCCAGCCTCT 60

Qy    2894 acgctgccccctggttcctcaccatgtttgcctcacagttcccgctgggattcgtagcca 2953
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ACGCTGCCCCCTGGTTCCTCACCATGTTTGCCTCACAGTTCCCGCTGGGATTCGTAGCCA 120

Qy    2954 gagtctttgatatgatttttcttcagggaacagaggtcatatttaaagtggctttaagtc 3013
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GAGTCTTTGATATGATTTTTCTTCAGGGAACAGAGGTCATATTTAAAGTGGCTTTAAGTC 180
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Qy   3014 tgttgggaagccataagcccttgattctgcagcatgaaaacctagaaaccatagttgact 3073
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TGTTGGGAAGCCATAAGCCCTTGATTCTGCAGCATGAAAACCTAGAAACCATAGTTGACT 240

Qy   3074 ttataaaaagcacgctacccaaccttggcttggtacagatggaaaagaccatcaatcagg 3133
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TTATAAAAAGCACGCTACCCAACCTTGGCTTGGTACAGATGGAAAAGACCATCAATCAGG 300

Qy   3134 tatttgaaatggacatcgctaaacagttacaagcttatgaagttgagtaccacgtccttc 3193
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TATTTGAAATGGACATCGCTAAACAGTTACAAGCTTATGAAGTTGAGTACCACGTCCTTC 360

Qy   3194 aagaagaacttatcgattcctctcctctcagtgacaaccaaagaatggataaattagaga 3253
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AAGAAGAACTTATCGATTCCTCTCCTCTCAGTGACAACCAAAGAATGGATAAATTAGAGA 420

Qy   3254 aaaccaacagcagcttacgcaaacagaaccttgacctccttgaacagttgcaggtggcaa 3313
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AAACCAACAGCAGCTTACGCAAACAGAACCTTGACCTCCTTGAACAGTTGCAGGTGGCAA 480

Qy   3314 atggtaggatccaaagccttgaggccaccattgagaagctcctgagcagtgagagcaagc 3373
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 ATGGTAGGATCCAAAGCCTTGAGGCCACCATTGAGAAGCTCCTGAGCAGTGAGAGCAAGC 540

Qy   3374 tgaagcaggccatgcttaccttagaactggagcggtcggccctgctgcagacggtggagg 3433
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TGAAGCAGGCCATGCTTACCTTAGAACTGGAGCGGTCGGCCCTGCTGCAGACGGTGGAGG 600

Qy   3434 agctgcggcggcggagcgcagagcccagcgaccgggagcctgagtgcacgcagcccgagc 3493
          |||||||||||||| :||||||||||||||||||||||||||||||||||||||||||||
Db    601 AGCTGCGGCGGCGGA-SGCAGAGCCCAGCGACCGGGAGCCTGAGTGCACGCAGCCCGAGC 659

Qy   3494 ccacgggcgactgacagctctgcaggagagattgcaacaccatcccacactgtccaggcc 3553
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    660 CCACGGGCGACTGACAGCTCTGCAGGAGAGATTGCAACACCATCCCACACTGTCCAGGCC 719

Qy   3554 tt 3555
          ||
Db    720 TT 721


RESULT  14
BE300005
LOCUS       BE300005               754 bp    mRNA    linear   EST 20-JUL-2000
DEFINITION  600944594F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960783 5',
            mRNA sequence.
ACCESSION   BE300005
VERSION     BE300005.1  GI:9183753
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 754)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM54  row: k  column: 24
            High quality sequence start: 2
            High quality sequence stop: 753.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:2960783"
                     /clone_lib="NIH_MGC_17"
                     /tissue_type="rhabdomyosarcoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
                     Site_2: XhoI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G).  Size-selected >500bp
                     for average insert size 1.8kb.  Library constructed by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      227 a    186 c    177 g    164 t
ORIGIN


  Query Match             19.2%;  Score 683.4;  DB 10;  Length 754;
  Best Local Similarity   99.1%;  Pred. No. 7.5e-160;
  Matches  750;  Conservative    0;  Mismatches    1;  Indels    6;  Gaps    6;

Qy   1878 ctcagtgagcacagagacgcctcatgaacgaaaggactttgaatccaaagcaaaccatct 1937
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CTCAGTGAGCACAGAGACGCCTCATGAACGAAAGGACTTTGAATCCAAAGCAAACCATC- 59

Qy   1938 tggtgattctggtgggactcctgtgaagacccggaggcattcctggaggcagcagatatt 1997
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     60 TGGTGATTCTGGTGGGACTCCTGTGAAGACCCGGAGGCATTCCTGGAGGCAGCAGATATT 119

Qy   1998 cctccgagtagccaccccgcagaaggcgtgcgattcttccagcagatatgaagattattc 2057
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    120 CCTCCGAGTAGCCACCCCGCAGAAGGCGTGCGATTCTTCCAGCAGATATGAAGATTATTC 179

Qy   2058 agagctgggagagcttcccccacgatctcctttagaaccagtttgtgaagatgggccctt 2117
          |||||||||||||||||||||||||||||||||||||||| |||||||||||||||| |
Db    180 AGAGCTGGGAGAGCTTCCCCCACGATCTCCTTTAGAACCAG-TTGTGAAGATGGGCCC-T 237

Qy   2118 tggccccccaccagaggaaaagaaaaggacatctcgtgagctccgagagctgtggcaaaa 2177
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    238 TGGCCCCCCACCAGAGGAAAAGAAAAGGACATCTCGTGAGCTCCGAGAGCTGTGGCAAAA 297

Qy   2178 ggctattcttcaacagatactgctgcttagaatggagaaggaaaatcagaagctccaagc 2237
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    298 GGCTATTCTTCAACAGATACTGCTGCTTAGAATGGAGAAGGAAAATCAGAAGCTCCAAGC 357

Qy   2238 ctctgaaaatgatttgctgaacaagcgcctgaagctcgattatgaagaaattactccctg 2297
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    358 CTCTGAAAATGA-TTGCTGAACAAGCGCCTGAAGCTCGATTATGAAGAAATTACTCCCTG 416

Qy   2298 tcttaaagaagtaactacagtgtgggaaaagatgcttagcactccaggaagatcaaaaat 2357
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    417 TCTTAAAGAAGTAACTACAGTGTGGGAAAAGATGCTTAGCACTCCAGGAAGATCAAAAAT 476

Qy   2358 taagtttgacatggaaaaaatgcactcggctgttgggcaaggtgtgccacgtcatcaccg 2417
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    477 TAAGTTTGACATGGAAAAAATGCACTCGGCTGTTGGGCAAGGTGTGCCACGTCATCACCG 536

Qy   2418 aggtgaaatctggaaatttctagctgagcaattccaccttaaacaccagtttcccagcaa 2477
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    537 AGGTGAAATCTGGAAATTTCTAGCTGAGCAATTCCACCTTAAACACCAGTTTCCCAGCAA 596

Qy   2478 acagcagccaaaggatgtgccatacaaagaactcttaaagcagctgacttcccagcagca 2537
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    597 ACAGCAGCCAAAGGATGTGCCATACAAAGAACTCTTAAAGCAGCTGACTTCCCAGCAGCA 656

Qy   2538 tgcgattcttattgaccttgggcgaacctttcctacacacccatacttctctgcccagct 2597
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    657 TGCGATTCTTA-TGACCTTGGGCGAACCTTTCCTACACACCCATACTTCTCTGCCCAGCT 715

Qy   2598 tggagcaggacagctatcgctttacaacattttgaag 2634
          |||||||||||||||||| |||||||||||||| |
Db    716 TGGAGCAGGACAGCTATCGC-TTACAACATTTTGAGG 751


RESULT  15
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BE561889
LOCUS       BE561889                892 bp    mRNA    linear   EST 15-AUG-2000
DEFINITION  601346094F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3678887 5',
            mRNA sequence.
ACCESSION   BE561889
VERSION     BE561889.1  GI:9805609
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 892)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM356  row: l  column: 24
            High quality sequence start: 50
            High quality sequence stop: 758.
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                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      224 a    240 c    242 g    186 t
ORIGIN
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Query Match 19.2%; Score 682.6; DB 10; Length 892;
Best Local Similarity 95.3%; Pred. No. 1.3e-159;
Matches 790; Conservative 0; Mismatches 29; Indels 10; Gaps 8;

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Qy   1628 aagagccatctgtgtgtgaaaaggaggccttgcccatctctgagagctcctttaagctcc 1687
          ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db     63 AAGAGCCATCTGTGTGTGAAAAGGAGG-CTTGCCCATCTCTGAGAGCTCCTTTAAGCTCC 121

Qy   1688 tcggctcctcggaggacctgtccagtgactcggagagtcatctcccagaagagccagctc 1747
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    122 TCGGCTCCTCGGAGGACCTGTCCAGTGACTCGGAGAGTCATCTCCCAGAAGAGCCAGCTC 181

Qy   1748 cgctgtcgccccagcaggccttcaggaggcgagcaaacaccctgagtcactt-ccccatc 1806
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Db    182 CGCTGTCGCCCCAGCAGGCCTTCAGGAGGCGAGCAAACACCCTGAGTCACTTCCCCCATC 241

Qy   1807 gaatgccaggaacctccacaacctgcccgggggtccccgggggtttcgcaaaggaaacttt 1866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    242 GAATGCCAGGAACCTCCACAACCTGCCCGGGGGTCCCCGGGGGTTTCGCAAAGGAAACTT 301

Qy   1867 atgaggtatcactcagtgagcacagagacgcctcatgaacgaaaggactttgaatccaaa 1926
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    302 ATGAGGTATCACTCAGTGAGCACAGAGACGCCTCATGAACGAAAGGACTTTGAATCCAAA 361

Qy   1927 gcaaaccatcttggtgattctggtgggactcctgtgaagacccggaggcattcctggagg 1986
          |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    362 GCAAATTATCTTGGTGATTCTGGTGGGACTCCTGTGAAGACCCGGAGGCATTCCTGGAGG 421

Qy   1987 cagcagatattcctccgagtagccaccccgcagaaggcgtgcgattcttccagcagatat 2046
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    422 CAGCAGATATTCCTCCGAGTAGCCACCCCGCAGAAGGCGTGCGATTCTTCCAGCAGATAT 481

Qy   2047 gaagattattcagagctgggagagcttcccccacgatctcctttagaaccagtttgtgaa 2106
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    482 GAAGATTATTCAGAGCTGGGAGAGCTTCCCCCACGATCTCCTTTAGAACCAGTTTGTGAA 541

Qy   2107 gatgggccctttggccccccaccagaggaaaagaaaaggacatctcgtgagctccgagag 2166
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    542 GATGGGCCCTTTGGCCCCCCACCAGAGGAAACGAAAAGGACATCTCGTGAGCTCCGAGAG 601

Qy   2167 ctgtggcaaaaggctattcttcaacagatactgctgcttagaatggagaaggaaaatcag 2226
          |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    602 CTGTGGCAAAAGGCTATTCTTCAACAGATACTGCTGCTTAGAATGGCGAAGGAAAATCAG 661

Qy   2227 aagctccaagcctctgaaaatgatttgctgaacaagcgcctgaagctcgattatgaagaa 2286
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    662 AAGCTCCAAGCCTCTGAAAATGATTTGCTGAACAAGCGCCTGAAGCTCGATTATGAAGAA 721

Qy   2287 attactccctg-tcttaaagaagtaactacagtgtggga--aaagatgcttagcactcca 2343
          |||||||||||| ||||||||||||||||||||||||||  ||    ||||||||||||
Db    722 ATTACTCCCTGTTCTTAAAGAAGTAACTACAGTGTGGGACCAAGATGGCTTAGCACTCCA 781

Qy   2344 ggaagatcaaaaattaagtttgacatggaaaaaatgcactcggctgttgggcaaggtgtg 2403
          ||||||||    ||| |||||| | |||  | |||||  |||||  |||||||| ||| | |
Db    782 GGAAGATC-CCCATTTAGTTTGGCCTGGTGACAATGC-CTCGGGTGTTGGGCCAGGGGGG 839

Qy   2404 ccacgtcatcaccgaggtgaaatctggaaatttctagctgagcaattcc 2452
          || |||||||||| | |||||   ||  | || |||||| ||||||||
Db    840 CC-CGTCATCACCGCGCTGAAACTGGG--AGTTTTAGCTGGGCAATTCC 885
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: September 9, 2002, 14:27:02 ; Search time 706.85 Seconds
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8634.973 Million cell updates/sec

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Perfect score: 3555
Sequence: 1 atggaaccaataacattcac.....tcccacactgtccaggcctt 3555

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3555	100.0	3983	21	AAZ50906	Human TBC-1 cDNA f
2	3555	100.0	3988	21	AAZ50907	Human TBC-1 cDNA f
3	3026.4	85.1	3326	22	AAI57854	Human polynucleoti
4	2940.2	82.7	3727	21	AAC77404	Human ORFX ORF2959
5	2833.8	79.7	3281	22	AAI59640	Human polynucleoti
6	2510.4	70.6	4039	19	AAV05886	Human Tbc-1 gene.
7	2112	59.4	2362	22	AAH18401	Human cDNA sequenc
8	1000.8	28.2	1422	22	AAS34787	cDNA encoding nove
9	999.4	28.1	2989	22	AAK94796	Human full-length
10	943.2	26.5	1269	22	AAS34785	cDNA encoding nove
11	785	22.1	883	22	AAH04450	Human cDNA clone (
12	574.2	16.2	849	22	AAK92006	Human cDNA 5'-end
13	574.2	16.2	849	22	AAK93666	Human cDNA clone r
14	422.6	11.9	17590	21	AAZ50904	Human TBC-1 partia
15	362	10.2	696	20	AAZ15229	Human gene express
16	306.2	8.6	5472	23	ABL02013	Drosophila melanog
17	284.4	8.0	99960	21	AAZ50905	Human TBC-1 partia
18	280	7.9	458	20	AAX40323	Human secreted pro
c 19	245.6	6.9	8105	23	ABL02012	Drosophila melanog
c 20	228.4	6.4	555	22	AAH09958	Human cDNA clone (
21	132.8	3.7	3691	22	AAF58616	Human RECAP polynu
22	132.8	3.7	4827	22	AAI59592	Human polynucleoti
23	132.8	3.7	5294	22	AAI57806	Human polynucleoti
24	128.8	3.6	3585	23	ABL12337	Drosophila melanog
25	123.8	3.5	154	23	AAS58636	cDNA #1312 encodin
26	119.4	3.4	2626	23	ABL18133	Drosophila melanog
27	119.4	3.4	7829	23	ABL18132	Drosophila melanog
28	108	3.0	2424	23	AAS71793	DNA encoding novel
29	83.8	2.4	1601	21	AAC33401	Arabidopsis thalia
c 30	79.6	2.2	6765	23	ABL12336	Drosophila melanog
31	78.4	2.2	300	20	AAZ13067	Human gene express
32	75.2	2.1	1492	21	AAC38750	Arabidopsis thalia
c 33	73.8	2.1	1140	21	AAZ97020	Human secreted pro
34	68.4	1.9	3342	22	AAF32789	Human secreted pro
35	68	1.9	2492	21	AAC78199	Human cancer assoc
36	65.2	1.8	1831	22	AAH64964	Human secreted pro
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43	61.6	1.7	2801	22	AAF32643	Human cDNA encodin
c 44	61.6	1.7	2803	22	AAS27080	cDNA encoding nove
45	61.6	1.7	2903	22	AAK51641	Human polynucleoti

ALIGNMENTS

RESULT 1
AAZ50906
ID AAZ50906 standard; cDNA; 3983 BP.
XX
AC AAZ50906;
XX
DT 31-MAY-2000 (first entry)
XX
DE Human TBC-1 cDNA from first transcript.
XX
KW TBC-1; human; biallelic marker; chromosome 4; cell cycle regulator; SNP;
KW Single nucleotide polymorphism; tissue differentiation; prostate cancer;
KW linkage analysis; genetic map; detection; diagnosis; genotyping;
KW transgenic animal; screening; alternative splicing; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 5'UTR 1..170
FT /*tag= a
FT /note= "Spans through exon 1 and part of exon 2"
FT CDS 171..3677
FT /*tag= b
FT /product= "Human TBC-1 protein"
FT /note= "First transcription product"
FT 3'UTR 3726..3983
FT /*tag= c
FT polyA_signal 3942..3947
FT /*tag= d
XX
PN WO200008209-A2.
XX

PD 17-FEB-2000.
XX
PF 06-AUG-1999; 99WO-IB01444.
XX
PR 07-AUG-1998; 98US-0095653.
XX
PA (GEST) GENSET.
XX
PI Blumenfeld M, Bougueleret L, Chumakov I;
XX
DR WPI; 2000-205736/18.
DR P-PSDB; AAY45096.
XX
PT New isolated human TBC-1 nucleic acids, useful for developing products
PT for the diagnosis and treatment of disorders involving cell
PT proliferation, particularly prostate cancer -
XX
PS Claim 3; Page 150-155; 166pp; English.
XX
CC The present sequence is the cDNA encoding the first transcription
CC product of human TBC-1 protein, comprising exons 1-2 and A-L.
CC Alternative splicing events result in two mRNA molecules, due to
CC splicing at two distinct first exons, exon1 and exon 1bis. TBC-1 gene
CC is mapped to a candidate region of prostate cancer on chromosome 4.
CC TBC-1 gene is involved in the regulation of cell cycle and tissue
CC differentiation in mammals. An alteration of TBC-1 sequence may be
CC associated with a pathological condition, resulting in abnormal cell
CC proliferation leading to cancer, e.g. prostate cancer. The biallelic
CC markers can be used for generation of genetic maps, linkage analysis and
CC association studies. TBC-1 sequence can be used for detection,
CC diagnosis, genotyping, production of transgenic animals and screening
CC of compounds for use in therapy.
XX
SQ Sequence 3983 BP; 1090 A; 1007 C; 1007 G; 878 T; 1 other;

Query Match 100.0%; Score 3555; DB 21; Length 3983;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db   3051 ggccccagcctctacgctgccccctggttcctcaccatgtttgcctcacagttcccgctg 3110

Qy   2941 ggattcgtagccagagtctttgatatgatttttcttcagggaacagaggtcatatttaaa 3000
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Qy   3121 accatcaatcaggtatttgaaatggacatcgctaaacagttacaagcttatgaagttgag 3180
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Qy   3181 taccacgtccttcaagaagaacttatcgattcctctcctctcagtgacaaccaaagaatg 3240
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RESULT 2
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ID AAZ50907 standard; cDNA; 3988 BP.
XX
AC AAZ50907;
XX
DT 31-MAY-2000 (first entry)
XX
DE Human TBC-1 cDNA from second transcript.
XX
KW TBC-1; human; biallelic marker; chromosome 4; cell cycle regulator; SNP;

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KW   Single nucleotide polymorphism; tissue differentiation; prostate cancer;
KW   linkage analysis; genetic map; detection; diagnosis; genotyping;
KW   transgenic animal; screening; alternative splicing; ss.
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PD   17-FEB-2000.
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PF   06-AUG-1999;   99WO-IB01444.
XX
PR   07-AUG-1998;   98US-0095653.
XX
PA   (GEST ) GENSET.
XX
PI   Blumenfeld M,  Bougueleret L,  Chumakov I;
XX
DR   WPI; 2000-205736/18.
DR   P-PSDB; AAY45096.
XX
PT   New isolated human TBC-1 nucleic acids, useful for developing products
PT   for the diagnosis and treatment of disorders involving cell
PT   proliferation, particularly prostate cancer -
XX
PS   Claim 4; Page 156-161; 166pp; English.
XX
CC   The present sequence is the cDNA encoding the second transcription
CC   product of human TBC-1 protein, comprising exons 1bis to 2 and A-L.
CC   Alternative splicing events result in two mRNA molecules, due to
CC   splicing at two distinct first exons, exon1 and exon 1bis. TBC-1 gene
CC   is mapped to a candidate region of prostate cancer on chromosome 4.
CC   TBC-1 gene is involved in the regulation of cell cycle and tissue
CC   differentiation in mammals. An alteration of TBC-1 sequence may be
CC   associated with a pathological condition, resulting in abnormal cell
CC   proliferation leading to cancer, e.g. prostate cancer. The biallelic
CC   markers can be used for generation of genetic maps, linkage analysis and
CC   association studies. TBC-1 sequence can be used for detection,
CC   diagnosis, genotyping, production of transgenic animals and screening
CC   of compounds for use in therapy.
XX
SQ   Sequence 3988 BP; 1107 A; 983 C; 1002 G; 896 T; 0 other;


  Query Match             100.0%;  Score 3555;  DB 21;  Length 3988;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 3555;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     61 tttggcctgcagctggtgggctccctgcctgtgcattccctgaccaccatgcccatgctg 120
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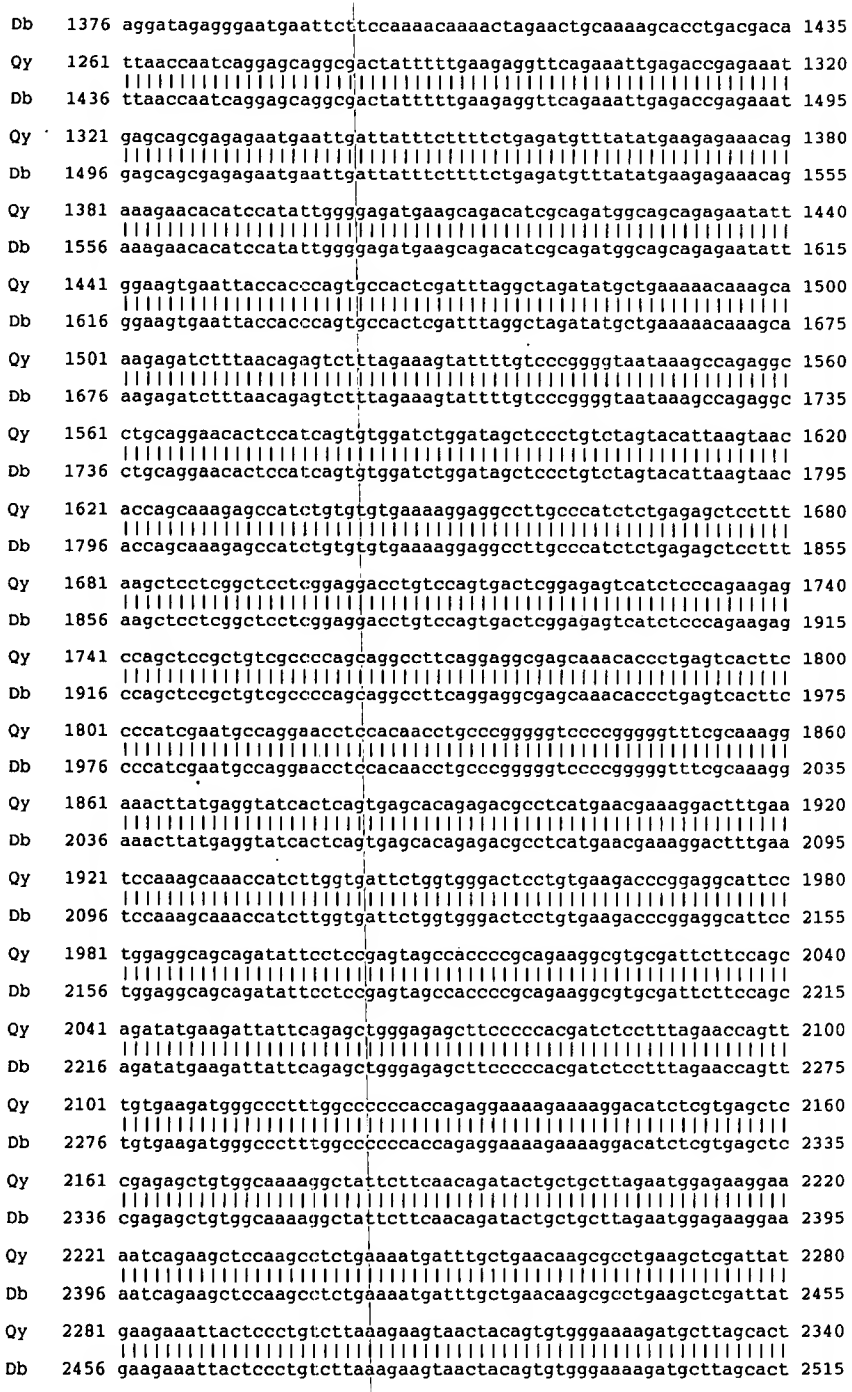
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RESULT   3
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DT   22-OCT-2001  (first entry)
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KW   peripheral nervous system; neuropathy; central nervous system; CNS;
KW   Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW   amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW   chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW   leukaemia; ss.
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OS   Homo sapiens.
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PD   26-JUL-2001.
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PF   26-DEC-2000; 2000WO-US34263.
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PR   21-JAN-2000; 2000US-0488725.
PR   25-APR-2000; 2000US-0552317.
PR   09-JUL-2000; 2000US-0598042.
PR   19-JUL-2000; 2000US-0620312.
PR   03-AUG-2000; 2000US-0653450.
PR   14-SEP-2000; 2000US-0662191.
PR   19-OCT-2000; 2000US-0693036.
PR   29-NOV-2000; 2000US-0727344.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Asundi V,  Chen R,  Ma Y,  Qian XB,  Ren F,  Wang D;
PI   Wang J,  Wang Z,  Wehrman T,  Xu C,  Xue AJ,  Yang Y,  Zhang J;
PI   Zhao QA,  Zhou P,  Goodrich R,  Drmanac RT;
XX
DR   WPI; 2001-442253/47.
DR   P-PSDB; AAM38698.
XX
PT   Novel nucleic acids and polypeptides, useful for treating disorders
PT   such as central nervous system injuries -  .
XX
PS   Claim 1; SEQ ID NO 57; 10078pp; English.
XX
CC   The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC   the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC   immunosuppressant and cytostatic activity. The polynucleotides are useful
CC   in gene therapy. A composition containing a polypeptide or polynucleotide
CC   of the invention may be used to treat diseases of the peripheral nervous
CC   system, such as peripheral nervous injuries, peripheral neuropathy and
CC   localised neuropathies and central nervous system diseases, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC   utilisation of the activities such as: Immune system suppression,
CC   Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC   assays for receptor activity, arthritis and inflammation, leukaemias and
CC   C.N.S disorders.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification.
XX
SQ   Sequence 3326 BP; 924 A; 824 C; 843 G; 735 T; 0 other;


  Query Match             85.1%;  Score 3026.4;  DB 22;  Length 3326;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 3030;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

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Qy    580 gacgagtgcatcgagaagttcaatcacgtcagcggcagccgggggtccgagagccccccgc 639
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Qy    640 cccaacccgccccatgccgcgcccacagggagccaggagcctgtgcgcaggcccatgcgc 699
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Qy    760 ggcctccgaagcagcggcttcttcagctccttcgaggagagcgacattgagaaccacctc 819
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Qy    880 acgattggccagtctgaagtttacctcatcagtcctgacaccaaaaaaatagcattggag 939
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RESULT   4
AAC77404
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ID AAC77404 standard; cDNA; 3727 BP.
XX
AC AAC77404;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human ORFX ORF2959 polynucleotide sequence SEQ ID NO:5917.
XX
KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW- immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cholesterol ester storage; systemic lupus erythematosus; infection;
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW thrombosis; contraceptive; ss.
XX
OS Homo sapiens.
XX
PN WO200058473-A2.
XX
PD 05-OCT-2000.
XX
PF 31-MAR-2000; 2000WO-US08621.
XX
PR 31-MAR-1999; 99US-0127607.
PR 02-APR-1999; 99US-0127636.
PR 05-APR-1999; 99US-0127728.
PR 30-MAR-2000; 2000US-0540763.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2000-602362/57.
DR P-PSDB; AAB43195.
XX
PT Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease -
XX
PS Claim 5; Page 5094-5096; 5507pp; English.
XX
CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC sequences have activities such as: cytostatic; hepatotropic; vulnerary;
CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
CC antidiabetic; hypotensive; dermatological; immunosuppressive;
CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
CC antithyroid; and antianaemic. The sequences can be used for determining
CC the presence of or predisposition to, or preventing or treating
CC pathological conditions associated with an ORFX-associated disorder. The
CC nucleic acids can be used to express ORFX proteins in gene therapy
CC vectors. The proteins and nucleic acids may be used to treat cancers,
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC graft vs host disease, cardiovascular disease, diabetes mellitus,
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
CC coagulation; to inhibit thrombosis; and as a contraceptive.
XX
SQ Sequence 3727 BP; 1031 A; 889 C; 931 G; 875 T; 1 other;

Query Match 82.7%; Score 2940.2; DB 21; Length 3727;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 3005; Conservative 0; Mismatches 13; Indels 7; Gaps 5;

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Qy   2152 cgtgagctccgagagctgtggcaaaaggctattcttcaacagatactgc-tgcttagaat 2210
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Db   1623 cgtgagctccgagagctgtggcaaagggctattcttcaacagatactgcntgcttagaat 1682

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Qy   2331 gcttagcactccaggaagatcaaaaattaagtttgacatggaaaaaatgcactcggctgt 2390
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Qy   2691 aggcattttgcttcttcatatgagtgaggaagaggcgtttaaaatgctcaagtttctgat 2750
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Qy   2751 gtttgacatggggctgcggaaacagtatcggccagacatgattattttacagatccagat 2810
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Qy   3171 tgaagttgagtaccacgtccttcaagaagaacttatcgattcctctcctctcagtgacaa 3230
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Qy   3351 gctcctgagcagtgagagcaagctgaagcaggccatgcttaccttagaactggagcggtc 3410
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Qy   3471 gcctgagtgcacgcagcccgagcccacgggcgactgacagctctgcaggagagattgcaa 3530
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RESULT   5
AAI59640
ID   AAI59640 standard; cDNA; 3281 BP.
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AC   AAI59640;
XX
DT   22-OCT-2001  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 3629.
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KW   Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW   peripheral nervous system; neuropathy; central nervous system; CNS;
KW   Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW   amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW   chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW   leukaemia; ss.
XX
OS   Homo sapiens.
XX
PN   WO200153312-A1.
XX
PD   26-JUL-2001.
XX
PF   26-DEC-2000; 2000WO-US34263.
XX
PR   21-JAN-2000; 2000US-0488725.
PR   25-APR-2000; 2000US-0552317.
PR   09-JUL-2000; 2000US-0598042.
PR   19-JUL-2000; 2000US-0620312.
PR   03-AUG-2000; 2000US-0653450.
PR   14-SEP-2000; 2000US-0662191.
PR   19-OCT-2000; 2000US-0693036.
PR   29-NOV-2000; 2000US-0727344.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Asundi V,  Chen R,  Ma Y,  Qian XB,  Ren F,  Wang D;
PI   Wang J,  Wang Z,  Wehrman T,  Xu C,  Xue AJ,  Yang Y,  Zhang J;
PI   Zhao QA,  Zhou P,  Goodrich R,  Drmanac RT;
XX
DR   WPI; 2001-442253/47.
DR   P-PSDB; AAM40484.
XX
PT   Novel nucleic acids and polypeptides, useful for treating disorders
PT   such as central nervous system injuries -
XX
PS   Claim 1; SEQ ID NO 3629; 10078pp; English.
XX
CC   The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC   the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC   immunosuppressant and cytostatic activity. The polynucleotides are useful
CC   in gene therapy. A composition containing a polypeptide or polynucleotide
CC   of the invention may be used to treat diseases of the peripheral nervous
CC   system, such as peripheral nervous injuries, peripheral neuropathy and
CC   localised neuropathies and central nervous system diseases, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC   utilisation of the activities such as: Immune system suppression,
CC   Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC   assays for receptor activity, arthritis and inflammation, leukaemias and
CC   C.N.S disorders.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification.
XX
SQ   Sequence 3281 BP; 912 A; 812 C; 824 G; 733 T; 0 other;


  Query Match             79.7%;  Score 2833.8;  DB 22;  Length 3281;
  Best Local Similarity   98.3%;  Pred. No. 0;
  Matches 2983;  Conservative    0;  Mismatches   32;  Indels   20;  Gaps   11;

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Qy    896 aagtttacctcatcagtcctgacaccaaaaaaat-----agcattggagaaaaattttaa 950
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Qy   1722 gagtcatctcccagaagagccagctccgctgtcgccccagcaggccttcaggaggcgagc 1781
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 acctggaggagcacgagatcggccccagcctctacgctgccccctggttcctcaccatgt 2400

Qy   2921 ttgcctcacagttcccgctgggattcgtagccagagtctttgatatgatttttcttcagg 2980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 ttgcctcacagttcccgctgggattcgtagccagagtctttgatatgatttttcttcagg 2460

Qy   2981 gaacagaggtcatatttaaagtggctttaagtctgttgggaagccataagcccttgattc 3040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 gaacagaggtcatatttaaagtggctttaagtctgttgggaagccataagcccttgattc 2520

Qy   3041 tgcagcatgaaaacctagaaaccatagttgactttataaaaagcacgctacccaaccttg 3100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 tgcagcatgaaaacctagaaaccatagttgactttataaaaagcacgctacccaaccttg 2580

Qy   3101 gcttggtacagatggaaaagaccatcaatcaggtatttgaaatggacatcgctaaacagt 3160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 gcttggtacagatggaaaagaccatcaatcaggtatttgaaatggacatcgctaaacagt 2640

Qy   3161 tacaagcttatgaagttgagtaccacgtccttcaagaagaacttatcgattcctctcctc 3220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 tacaagcttatgaagttgagtaccacgtccttcaagaagaacttatcgattcctctcctc 2700

Qy   3221 tcagtgacaaccaaagaatggataaattagagaaaaccaacagcagcttacgcaaacaga 3280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 tcagtgacaaccaaagaatggataaattagagaaaaccaacagcagcttacgcaaacaga 2760

Qy   3281 accttgacctccttgaacagttgcaggtggcaaatggtaggatccaaagccttgaggcca 3340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 accttgacctccttgaacagttgcaggtggcaaatggtaggatccaaagccttgaggcca 2820

Qy   3341 ccattgagaagctcctgagcagtgagagcaagctgaagcaggccatgcttaccttagaac 3400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 ccattgagaagctcctgagcagtgagagcaagctgaagcaggccatgcttaccttagaac 2880

Qy   3401 tggagcggtcggccctgctgcagacggtggaggagctgcggcggcggagcgcagagccca 3460
          |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db   2881 tggagcggtcggccctgctgcagacggtggaggagctgcggcggcggagcgcaaagccca 2940

Qy   3461 gcgaccgggagcctgagtgcacgcagcccgagcccacgggcgactgacagctctgcagga 3520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 gcgaccgggagcctgagtgcacgcagcccgagcccacgggcgactgacagctctgcagga 3000

Qy   3521 gagattgcaacaccatcccacactgtccaggcctt 3555
          |||||||||||||||||||||||||||||||||||
Db   3001 gagattgcaacaccatcccacactgtccaggcctt 3035
```

RESULT 6
AAV05886
ID AAV05886 standard; DNA; 4039 BP.
XX
AC AAV05886;
XX
DT 01-JUN-1998 (first entry)
XX
DE Human Tbc-1 gene.
XX
KW tre-2; BUB2; cdc16; mast cell; probe; hybridisation; subtraction method;
KW mouse; transcription factor; differentiation; proliferation; human; ds;
KW acute myelogenous leukaemia.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 403..3828
FT /*tag= a
FT /product= Tbc1_protein
XX
PN US5700927-A.
XX
PD 23-DEC-1997.

XX
PF 23-DEC-1994; 94US-0363300.
XX
PR 23-DEC-1994; 94US-0363300.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Richardson P, Zon L;
XX
DR WPI; 1998-062437/06.
DR P-PSDB; AAW44777.
XX
PT DNA encoding Tbc1 polypeptide - useful for treating leukaemia
XX
PS Claim 3; Fig 1A-B; 22pp; English.
XX
CC This is the nucleotide sequence which encodes a Tbc1 (tre-2, BUB2 and
CC cdc16) polypeptide, isolated from a bone marrow-derived mast cell DNA
CC library. The screen was carried out using a probe generated by a
CC subtraction method which compared mRNA expression in an undifferentiated
CC mast cell line P815 and cell line PGT6 (P815 cells transformed to express
CC the murine GATA-1 transcription factor - a factor which controls the
CC expression of genes involved in mast cell differentiation). Tbc1 encodes
CC a protein involved in the coupling of cell proliferation to cell
CC differentiation, which can be used to treat leukaemia (especially acute
CC myelogenous leukaemia) by causing leukaemic cells to differentiate.
XX
SQ Sequence 4039 BP; 1042 A; 1096 C; 1060 G; 841 T; 0 other;

Query Match 70.6%; Score 2510.4; DB 19; Length 4039;
Best Local Similarity 83.7%; Pred. No. 0;
Matches 2949; Conservative 0; Mismatches 536; Indels 37; Gaps 8;

```
Qy      1 atggaaccaataacattcacagcaaggaaacatctgctt-cctaacgaggtctcggtgga 59
          |||||  |||| |||||||||| ||||| |||| | || |||||||| ||||| |||||
Db    292 atggaggcaatcacattcacagcgaggaagcatccgtttccctaacgaagtctccgtgga 351

Qy     60 ttttggcctgcagctggt--gggctccctgcctgtgcattccctgaccaccatgcccatg 117
           || ||| ||||||||||  |||||| | || |||||||| || ||||| |||||||||
Db    352 cttcggcttgcagctggttgggtctccttacccgtgcattctctcaccactatgcccatg 411

Qy    118 ctgccctgggttgtggctgaggtgcgaagactcagcaggcagtccaccagaaaggaacct 177
          ||||| ||||| || || ||||| ||||||||||  | |||| | | | |||||| |||
Db    412 ctgccgtgggtggtagccgaggtacgaagactcagtggccagtgctctaaaaaggagcct 471

Qy    178 gtaaccaagcaagtccggctttgcgtttcaccctctggactgagatgtgaacctgagcca 237
             || |||||||||| ||||| ||||| ||||| | | || || |||||  |
Db    472 aggacaaagcaagtccgcctttgggtttcgccctccggactgcggtgcgagcctgacctg 531

Qy    238 gggagaagtcaacagtgggatccccctgatctattccagcatctttgagtgcaagcctcag 297
          | || ||||||||  ||||| || || |||| ||||||||||||||||||||||||||||
Db    532 gagaaaagtcaaccatgggacccgctcatctgttccagcatctttgagtgcaagcctcag 591

Qy    298 cgtgttcacaaactgattcacaacagtcatgacccaagttactttgcttgtctgattaag 357
          ||||| |||||||||||||||||||||| ||||| || |||||||||| || ||||||
Db    592 cgtgtgcacaaactgattcacaacagtcacgacccgagctactttgcttgcctcattaag 651

Qy    358 gaagacgctgtccaccggcagagtatctgctatgtgttcaaagccgatgatcaaacaaaa 417
          || || |||| ||| |||||||| |||||||||||||| ||||| || ||||||||||||
Db    652 gaggatgctgcgcacaggcagagcctctgctatgtgtttaaagcagacgatcaaacaaaa 711

Qy    418 gtgcctgagatcatcagctccatccgtcaggcggggaagatcgcccggcaggaggagctg 477
          |||||||||||||||||||||||||| ||||| |||||||| |||||  ||||||
Db    712 gtgcctgagatcatcagctccatccggcaggccgggaagattgcccgccaggaagagctg 771

Qy    478 cactgcccgtccgagttcgacgacacgttttccaagaagttcgaggtgctcttctgcggc 537
          |  ||||| |||||||||||||| || ||  |||| ||||||||||||||||||| |||
Db    772 cgttgcccctccgagttcgacgataccttcgccaaaaagttcgaggtgctcttctgtggc 831

Qy    538 cgcgtgacggtggcgcacaagaaggctccgccggccctgatcgacgagtgcatcgagaag 597
          || ||||| ||||| |||||||||| || || || ||||| |||||||| |||||||||
Db    832 cgggtgactgtggctcacaagaaggccccacccgcactgattgacgagtgtatcgagaag 891

Qy    598 ttcaatcacgtcagcggcagccgggggtccgagagcccccgccccaacccgccccatgcc 657
          ||||| || || ||| |  | ||  |  | ||  |       |||| |  ||  |   |
Db    892 ttcaaccatgtgagctgtggtcgcagaacggactgggaagcgcccaccgggcagccatca 951

Qy    658 gcgcccacagggagccaggagcctgtgcgcaggcccatgcgcaagtccttctcccagccc 717
          ||                |||||  | ||||||||||||||| ||||||||  |||||
Db    952 gc------------------gcctggccccaggcccatgcgcaaatccttctcacagcct 993

Qy    718 ggcctgcgctcgctggcctttaggaaggagctgcaggatgggggcctccgaagcagcggc 777
          || |||||||||||||||| ||||||||| | ||||| |   ||||||| || |||  |
Db    994 ggactgcgctcgctggccttcaggaaggagttccaggacgctagcctccgcagtagcacc 1053

Qy    778 ttcttcagctccttcgaggagagcgacattgagaaccacctcattagcggacacaatatt 837
          ||         || |   || |  ||||| ||||||||||||||  | || ||||||  |
Db   1054 tt------tagctcctttgacaatgacatagagaaccacctcatcggtgggcacaatgtg 1107

Qy    838 gtgcagcccacagatatcgaggaaaatcgaactatgctcttcacgattggccagtctgaa 897
          || |||||||||| || ||||| || |||||||||| ||||||||||||  ||||||
Db   1108 gttcagcccacagacatggaggagaaccgaactatgctgttcacgattggcccatctgaa 1167

Qy    898 gtttacctcatcagtcctgacaccaaaaaaatagcattggagaaaaatttttaaggagata 957
          |||||||||||||||||||||||||||||| || ||| ||||||||||||||||||||||
Db   1168 gtttacctcatcagtcctgacaccaaaaagattgcactggagaaaaatttttaaggagata 1227

Qy    958 tccttttgctctcagggcatcagacacgtggaccactttgggtttatctgtcgggagtct 1017
          |||||||||||||||||||||||||||||| |||||||||||||| || ||||| || ||||
Db   1228 tccttttgctctcagggcatcagacatgtggaccactttggattcatctgccgagagtgc 1287

Qy   1018 tc------cggaggtggcggctttcattttgtctgttacgtgtttcagtgcacaaatgag 1071
          ||      |||  ||||||||||||||||||||||||||||||||| ||||||||||||||
Db   1288 tcgggtggcggcagtggcggctttcattttgtctgttacgtgttccagtgcacaaatgaa 1347

Qy   1072 gctctggttgatgaaattatgatgaccctgaaacaggccttcacggtggccgcagtgcag 1131
          |||||||||||  || || |||||||| ||||| ||||| |||||||| || || ||||||
Db   1348 gctctggttgacgagatcatgatgactctgaagcaggctttcacggtagctgcggtgcag 1407

Qy   1132 cagacagctaaggcgccagcccagctgtgtgagggctgccccctgcaaagcctgcacaag 1191
          ||||| |||||||| |||||||||| |||||||||||||||| ||||| ||||||||||
Db   1408 cagacggctaaggcaccagcccagctctgtgagggctgccccttgcaaggcctgcacaag 1467

Qy   1192 ctctgtgagaggatagagggaatgaattcttccaaaacaaaactagaactgcaaaagcac 1251
          ||||| || |||||||||||||||||||| || ||||| ||| ||||||| || ||||||
Db   1468 ctctgcgaaaggatagagggaatgaattcatctaaaaccaaattagaactccagaagcac 1527

Qy   1252 ctgacgacattaaccaatcaggagcaggcgactatttttgaagaggttcagaaattgaga 1311
            |||| ||| | |||||||||||||||||| || || || || ||||||||||||||||||
Db   1528 ttgaccacactgaccaatcaggagcaggccaccatattcgaggaggttcagaaattgaga 1587

Qy   1312 ccgagaaatgagcagcgagagaatgaattgattatttcttttctgagatgtttatatgaa 1371
          || ||||| |||||||||||||||||||||| |||||||||||||||| || |||||||||
Db   1588 ccaagaaacgagcagcgagagaatgaattaattatttcttttctgaggtgcttatatgaa 1647

Qy   1372 gagaaacagaaagaacacatccatattggggagatgaagcagacatcgcagatggcagca 1431
          ||||| || ||||| |||| ||| | ||||| |   |||||||||   ||| ||||||||
Db   1648 gagaagcaaaaagagcacagccacactggggcgccaaagcagacactacaggtggcagca 1707

Qy   1432 gagaatattggaagtgaattaccacccagtgccactcgatttaggctagatatgctgaaa 1491
          |||||||||| |||||  | |||||||||| |  || || ||| |||||  ||||||
Db   1708 gagaatattgggagtgacctgccacccagtgctagccggttcaggttagattcgctgaag 1767

Qy   1492 aacaaagcaaagagatctttaacagagtctttagaaagtattttgtcccggggtaataaa 1551
          ||||  |||||||||| || ||||||||||  |||| || ||| ||||||||||||||||
Db   1768 aacagagcaaagaggtccttaacagagtccctagagagcattctgtcccggggtaataaa 1827

Qy   1552 gccagaggcctgcaggaacactccatcagtgtggatctggatagctccctgtctagtaca 1611
          |||||||||||||||| || |||  |||||||||||||| ||||||   ||||||||
Db   1828 gccagaggcctgcaggaccattccgccagtgtggatctggacagctccacttctagtact 1887

Qy   1612 ttaagtaacaccagcaaagagccatctgtgtgtgaaaaggaggccttgcccatctctgag 1671
            ||||||||||||||||||||  ||  || |||| |||||||||| ||| ||||||||
Db   1888 ctaagtaacaccagcaaagagctgtccatgggtgacaaggaggccttccccgtctctgag 1947
```

```
Qy   1672 agctcctttaagctcctcggctcctcggaggacctgtccagtgactcggagagtcatctc 1731
Db   1948 acctccttcaagctccttggctcctcagatgacctgtccagtgactcagagggccacatt 2007

Qy   1732 ccagaagagccagctccgctgtcgccccagcaggccttcaggaggcgagcaaacaccctg 1791
Db   2008 gcagaagagtctgccctgttgtcaccccagcaggcgttcagaaggagagccaacaccctg 2067

Qy   1792 agtcacttccccatcgaatgccaggaacctccacaacctgcccgggggtccccgggggtt 1851
Db   2068 agtcatttcccagtagagtgccctgcgcctccagaacctgcccagagctctccaggggtc 2127

Qy   1852 tcgcaaaggaaacttatgaggtatcactcagtgagcacagagacgcctcatgaacgaaag 1911
Db   2128 tctcaaaggaaactcatgcggtaccactccgtgagcacagagacgcctcatgaacgcaag 2187

Qy   1912 gactttgaatccaaagcaaaccatcttggtgattctggtgggactcctgtgaagacccgg 1971
Db   2188 gactttgaatccaaagcaaaccacctgggtgacacagatgggacccccgtgaagacccgg 2247

Qy   1972 aggcattcctggaggcagcagatattcctccgagtagccacccccgcagaaggcgtgcgat 2031
Db   2248 cggcactcgtggagacagcagatattccttcgagtggccactccacagaaggcttgtgac 2307

Qy   2032 tcttccagcagatatgaagattattcagagctgggagagcttcccccacgatctccttta 2091
Db   2308 tccccgagcagatatgaagattattccgagctgggagagctccctccacgctcccctttta 2367

Qy   2092 gaaccagtttgtgaagatgggccctttggcccccaccagaggaaaagaaaaggacatct 2151
Db   2368 gaaccggtgtgtgaggacggcccatttgg-ccagtacaggaagaaaagaggaagacgtca 2426

Qy   2152 cgtgagctccgagagctgtggcaaaaggctattcttcaacagatactg-ctgcttagaat 2210
Db   2427 cgcgagcttcgagagctgtggaaaaaggccatcttgcagcagatcctgcctcgtcaggat 2486

Qy   2211 ggagaaggaaaatcagaagctccaagcctctgaaaatgatttgctgaacaagcgcctgaa 2270
Db   2487 ggagaaggagaatcagaagctacaagcctctgaaaacgatttgctgaacaaacgcctcaa 2546

Qy   2271 gctcgattatgaagaaattactccctgtcttaaagaagtaactacagtgtgggaaaagat 2330
Db   2547 gcttgactatgaagaaatcactccgtgtcttaaagaagtcactacagtgtgggaaaagat 2606

Qy   2331 gcttagcactccaggaagatcaaaaattaagtttgacatggaaaaaatgcactcggctgt 2390
Db   2607 gcttagcactccaggaagatccaaaattaagtttgacatggaaaaagtgcactcagctgt 2666

Qy   2391 tgggcaaggtgtgccacgtcatcaccgaggtgaaatctggaaatttctagctgagcaatt 2450
Db   2667 tgggcaaggtgtgccacgtcatcaccgaggtgagatctggaaatttctagctgagcagtt 2726

Qy   2451 ccaccttaaacaccagtttcccagcaaacagcagccaaaggatgtgccatacaaagaact 2510
Db   2727 ccaccttaaacacccatttcctagtaaacagcagccaaaggacgtgccctacaaagagct 2786

Qy   2511 cttaaagcagctgacttcccagcagcatgcgattcttattgaccttgggcgaacctttcc 2570
Db   2787 cctgaagaagctgacctcgcagcagcacgccattctcatcgacctcgggcgaacctttcc 2846

Qy   2571 tacacacccatacttctctgcccagcttggagcaggacagctatcgctttacaacatttt 2630
Db   2847 aacacatccatacttctctgcccagcttggagcaggtcagctgtcactttacaacattct 2906

Qy   2631 gaaggcctactcacttctagaccaggaagtgggatattgccaaggtctcagctttgtagc 2690
Db   2907 gaaggcctactcgcttctggaccaggaggttggatactgccaaggtctcagctttgtggc 2966

Qy   2691 aggcattttgcttcttcatatgagtgaggaagaggcgtttaaaatgctcaagtttctgat 2750
Db   2967 aggcattttgcttcttcacatgagtgaggaagaggcgttcaagatgctcaagttcctgat 3026

Qy   2751 gtttgacatggggctgcggaaacagtatcggccagacatgattattttacagatccagat 2810
Db   3027 gtttgacatggggctgcggaaacagtatcggccagacatgattattttgcagatccagat 3086

Qy   2811 gtaccagctctcgaggttgcttcatgattaccacagagacctctacaatcacctggagga 2870
Db   3087 gtaccagctgtcacggctcctccacgattaccaccgagacctctacaaccacctggaaga 3146

Qy   2871 gcacgagatcggccccagcctctacgctgccccctggttcctcaccatgtttgcctcaca 2930
Db   3147 gcacgagactggccccctacgtacgcggctccctggtttctcaccgtgttcgcctcaca 3206

Qy   2931 gttcccgctgggattcgtagccagagtctttgatatgatttttcttcagggaacagaggt 2990
Db   3207 gttcccactcggctttgtagccagagtctttgatatgatcttccttcagggatcagaggt 3266

Qy   2991 catatttaaagtggctttaagtctgttgggaagccataagcccttgattctgcagcatga 3050
Db   3267 catatttaaagtagctttaagtcttttggggagccataagcccttgattctacagcatga 3326

Qy   3051 aaacctagaaaccatagttgactttataaaaagcacgctacccaaccttggcttggtaca 3110
Db   3327 gaacctggaaaccatcgtggacttcataaagaacacactccccaacctgggcctggtgca 3386

Qy   3111 gatggaaaagaccatcaatcaggtatttgaaatggacatcgctaaacagttacaagctta 3170
Db   3387 gatggagaagaccatcagtcaggtgtttgagatggacatcgccaagcagctccaggccta 3446

Qy   3171 tgaagttgagtaccacgtccttcaagaagaacttatcgattcctctcctctcagtgacaa 3230
Db   3447 tgaggtcgagtaccacgtcgtccaggaggagcttattgagtcctcgcctctcagtgacaa 3506

Qy   3231 ccaaagaatggataaattagagaaaaccaacagcagcttacgcaaacagaaccttgacct 3290
Db   3507 ccaaagaatggagaaattggagaaaaccaacagcacgttgcgcaaacagaaccttgacct 3566

Qy   3291 ccttgaacagttgcaggtggcaaatggtaggatccaaagccttgaggccaccattgagaa 3350
Db   3567 cctggagcagttgcaggtggcaaatgctaggatccaaagccttgaagccacggtagagaa 3626

Qy   3351 gctcctgagcagtgagagcaagctgaagcaggccatgcttaccttagaactggagcggtc 3410
Db   3627 acttcttaccagcgagagtaagctgaagcagcgtgcgctgaccctggaggtggagcg--t 3684

Qy   3411 ggccctgctgcagacggtggaggagctgcggcggcggagcgcagagcccagcgaccggga 3470
Db   3685 cgccctgctgcagatggtggaggagctgcggaggcaaagcgcccggcccagcactccaga 3744

Qy   3471 gcctgagtgcacgcagcccgagcccacgggcgactgacagct 3512
Db   3745 gccagactgcacccagctggagcccacaggcgattgaccgct 3786
```

```
RESULT   7
AAH18401
ID   AAH18401 standard; cDNA; 2362 BP.
XX
AC   AAH18401;
XX
DT   26-JUN-2001  (first entry)
XX
DE   Human cDNA sequence SEQ ID NO:18465.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-0116126.
XX
PR   29-JUL-1999;   99JP-0248036.
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PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
PS Claim 8; SEQ ID 18465; 2537pp + CD ROM; English.
XX
CC The present invention describes primer sets for synthesising 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.
XX
SQ Sequence 2362 BP; 657 A; 581 C; 578 G; 546 T; 0 other;

Query Match 59.4%; Score 2112; DB 22; Length 2362;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DT   04-DEC-2001  (first entry)
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KW   hyperproliferative disorder; neural disorder; immune system disorder;
KW   muscular disorder; reproductive disorder; gastrointestinal disorder;
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KW   neuroprotective; cytostatic; anti inflammatory; vasotropic; ss.
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OS   Homo sapiens.
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PN   WO200155163-A1.
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PD   02-AUG-2001.
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XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-465558/50.
DR P-PSDB; AAU21588.
XX
PT Novel polypeptides and polynucleotides useful as diagnostic reagents to
PT diagnose diseases or disorders associated with aberrant expression or
PT activity of polypeptides, and for treating cancers, rheumatoid
PT arthritis -
XX
PS Claim 4; SEQ ID No 31; 687pp; English.
XX
CC The present invention relates to the isolation of novel human neoplastic
CC disease associated polypeptides (AAU21568-AAU21851), and cDNA and DNA
CC sequences encoding for these polypeptides. The sequences of the
CC invention are useful in the diagnosis, treatment, prevention and/or
CC prognosis of disorders involving neoplastic disease such as
CC hyperproliferative disorders (e.g. leukaemia, bone cancer, bladder
CC cancer, brain stem glioma, adult liver cancer, childhood cerebellar
CC astrocytoma, or Hodgkin's lymphoma). The sequences of the invention may
CC also be useful for treating other disorders such as neural disorders,
CC immune system disorders, muscular disorders, reproductive disorders,
CC gastrointestinal disorders, pulmonary disorders, cardiovascular disorders
CC and renal disorders. The polynucleotide sequences of the invention are
CC also useful in gene therapy. AAS34767-AAS35050 represent cDNA sequences
CC encoding for the novel human neoplastic disease associated polypeptides
CC of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
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Query Match 28.2%; Score 1000.8; DB 22; Length 1422;
Best Local Similarity 99.3%; Pred. No. 1.5e-262;
Matches 1005; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy   3384 catgcttaccttagaactggagcggtcggccctgctgcagacggtggaggagctgcggcg 3443
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Qy   3444 gcggagcgcagagcccagcgaccgggagcctgagtgcacgcagcccgagcccacgggcga 3503
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Db   1039 gcggagcgcagagcccagcgaccgggagcctgagtgcacgcagcccgagcccacgggcga 1098

Qy   3504 ctgacagctctgcaggagagattgcaacaccatcccacactgtccaggcctt 3555
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Db   1099 ctgacagctctgcaggagagattgcaacaccatcccacactgtccaggcctt 1150


RESULT   9
AAK94796
ID   AAK94796 standard; cDNA; 2989 BP.
XX
AC   AAK94796;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human full-length cDNA, SEQ ID NO: 3914.
XX
KW   Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
XX
OS   Homo sapiens.
XX
PN   EP1130094-A2.
XX
PD   05-SEP-2001.
XX
PF   07-JUL-2000; 2000EP-0114089.
XX
PR   08-JUL-1999;   99JP-0194486.
PR   11-JAN-2000; 2000JP-0118774.
PR   02-MAY-2000; 2000JP-0183765.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Nishikawa T,  Isogai T,  Hayashi K,  Ishii S,  Kawai Y;
PI   Wakamatsu A,  Sugiyama T,  Nagai K,  Kojima S,  Otsuki T,  Koga H;
XX
DR   WPI; 2001-524255/58.
DR   P-PSDB; AAM93840.
XX
PT   830 Primers useful for synthesizing full length cDNA clones and their
PT   use in genetic manipulation -
XX
PS   Claim 8; SEQ ID NO 3914; 1380pp + sequence listing; English.
XX
CC   The invention relates to primers for synthesising full length cDNA
CC   clones. 830 cDNA molecules encoding a human protein have been
CC   isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC   molecules have been determined. Primers for synthesising the full length
CC   cDNA are useful for clarifying the function of the protein encoded by
CC   the cDNA. The full length clones were obtained by construction of full
CC   length enriched cDNA libraries that were synthesised by the oligo-capping
CC   method. The primers enable the production of the full length cDNA easily
CC   without any special methods. The present sequence is a full length
CC   human cDNA of the invention.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in CD-ROM format directly from EPO.
XX
SQ   Sequence 2989 BP; 795 A; 656 C; 698 G; 840 T; 0 other;


  Query Match             28.1%;  Score 999.4;  DB 22;  Length 2989;
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  Matches 1000;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   2555 ttgggcgaacctttcctacacacccatacttctctgcccagcttggagcaggacagctat 2614
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Qy   2615 cgctttacaacattttgaaggcctactcacttctagaccaggaagtgggatattgccaag 2674
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Db    258 cgctttacaacattttgaaggcctactcacttctagaccaggaagtgggatattgccaag 317

Qy   2675 gtctcagctttgtagcaggcattttgcttcttcatatgagtgaggaagaggcgtttaaaa 2734
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Db    318 gtctcagctttgtagcaggcattttgcttcttcatatgagtgaggaagaggcgtttaaaa 377

Qy   2735 tgctcaagtttctgatgtttgacatggggctgcggaaacagtatcggccagacatgatta 2794
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Db    378 tgctcaagtttctgatgtttgacatggggctgcggaaacagtatcggccagacatgatta 437

Qy   2795 ttttacagatccagatgtaccagctctcgaggttgcttcatgattaccacagagacctct 2854
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Db    438 ttttacagatccagatgtaccagctctcgaggttgcttcatgattaccacagagacctct 497

Qy   2855 acaatcacctggaggagcacgagatcggccccagcctctacgctgccccctggttcctca 2914
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Db    498 acaatcacctggaggagcacgagatcggccccagcctctacgctgccccctggttcctca 557

Qy   2915 ccatgtttgcctcacagttcccgctgggattcgtagccagagtctttgatatgatttttc 2974
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Qy   2975 ttcagggaacagaggtcatatttaaagtggctttaagtctgttgggaagccataagccct 3034
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Qy   3035 tgattctgcagcatgaaaacctagaaaccatagttgactttataaaaagcacgctaccca 3094
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Qy   3095 accttggcttggtacagatggaaaagaccatcaatcaggtatttgaaatggacatcgcta 3154
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Db    738 accttggcttggtacagatggaaaagaccatcaatcaggtatttgaaatggacatcgcta 797

Qy   3155 aacagttacaagcttatgaagttgagtaccacgtccttcaagaagaacttatcgattcct 3214
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Db    798 aacagttacaagcttatgaagttgagtaccacgtccttcaagaagaacttatcgattcct 857

Qy   3215 ctcctctcagtgacaaccaaagaatggataaattagagaaaaccaacagcagcttacgca 3274
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Db    858 ctcctctcagtgacaaccaaagaatggataaattagagaaaaccaacagcagcttacgca 917

Qy   3275 aacagaaccttgacctccttgaacagttgcaggtggcaaatggtaggatccaaagccttg 3334
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Db    918 aacagaaccttgacctccttgaacagttgcaggtggcaaatggtaggatccaaagccttg 977

Qy   3335 aggccaccattgagaagctcctgagcagtgagagcaagctgaagcaggccatgcttacct 3394
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Db    978 aggccaccattgagaagctcctgagcagtgagagcaagctgaagcaggccatgcttacct 1037

Qy   3395 tagaactggagcggtcggccctgctgcagacggtggaggagctgcggcggcggagcgcag 3454
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Db   1038 tagaactggagcggtcggccctgctgcagacggtggaggagctgcggcggcggagcgcag 1097

Qy   3455 agcccagcgaccgggagcctgagtgcacgcagcccgagcccacgggcgactgacagctct 3514
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Qy   3515 gcaggagagattgcaacaccatcccacactgtccaggcctt 3555
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Db   1158 gcaggagagattgcaacaccatcccacactgtccaggcctt 1198


RESULT  10
AAS34785
ID   AAS34785 standard; cDNA; 1269 BP.
XX
AC   AAS34785;
XX
DT   04-DEC-2001  (first entry)
XX
DE   cDNA encoding novel human neoplastic disease associated polypeptide #19.
XX
KW   Human; neoplastic disease associated polypeptide; cancer; gene therapy;
KW   hyperproliferative disorder; neural disorder; immune system disorder;
KW   muscular disorder; reproductive disorder; gastrointestinal disorder;
KW   pulmonary disorder; cardiovascular disorder; renal disorder;
KW   neuroprotective; cytostatic; anti inflammatory; vasotropic; ss.
XX
OS   Homo sapiens.
XX
PN   WO200155163-A1.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US01358.
XX
PR   31-JAN-2000; 2000US-0179065.
PR   04-FEB-2000; 2000US-0180628.
PR   24-FEB-2000; 2000US-0184664.
PR   02-MAR-2000; 2000US-0186350.
PR   16-MAR-2000; 2000US-0189874.
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PR   07-JUN-2000; 2000US-0209467.
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PR   08-NOV-2000; 2000US-0246611.
PR   08-NOV-2000; 2000US-0246613.
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PR   17-NOV-2000; 2000US-0249214.
PR   17-NOV-2000; 2000US-0249215.
PR   17-NOV-2000; 2000US-0249216.
PR   17-NOV-2000; 2000US-0249217.
PR   17-NOV-2000; 2000US-0249218.
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PR   17-NOV-2000; 2000US-0249244.
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PR   17-NOV-2000; 2000US-0249264.
PR   17-NOV-2000; 2000US-0249265.
PR   17-NOV-2000; 2000US-0249297.
PR   17-NOV-2000; 2000US-0249299.
PR   17-NOV-2000; 2000US-0249300.
PR   01-DEC-2000; 2000US-0250160.
PR   01-DEC-2000; 2000US-0250391.
PR   05-DEC-2000; 2000US-0251030.
PR   05-DEC-2000; 2000US-0251988.
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PR   06-DEC-2000; 2000US-0251479.
PR   08-DEC-2000; 2000US-0251856.
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PR   08-DEC-2000; 2000US-0251989.
PR   08-DEC-2000; 2000US-0251990.
PR   11-DEC-2000; 2000US-0254097.
PR   05-JAN-2001; 2001US-0259678.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Barash SC,  Ruben SM;
XX
DR   WPI; 2001-465558/50.
DR   P-PSDB; AAU21586.
XX
PT   Novel polypeptides and polynucleotides useful as diagnostic reagents to
PT   diagnose diseases or disorders associated with aberrant expression or
PT   activity of polypeptides, and for treating cancers, rheumatoid
PT   arthritis  -
XX
PS   Claim 4; SEQ ID No 29; 687pp; English.
XX
CC   The present invention relates to the isolation of novel human neoplastic
CC   disease associated polypeptides (AAU21568-AAU21851), and cDNA and DNA
CC   sequences encoding for these polypeptides. The sequences of the
CC   invention are useful in the diagnosis, treatment, prevention and/or
CC   prognosis of disorders involving neoplastic disease such as
CC   hyperproliferative disorders (e.g. leukaemia, bone cancer, bladder
CC   cancer, brain stem glioma, adult liver cancer, childhood cerebellar
CC   astrocytoma, or Hodgkin's lymphoma). The sequences of the invention may
CC   also be useful for treating other disorders such as neural disorders,
CC   immune system disorders, muscular disorders, reproductive disorders,
CC   gastrointestinal disorders, pulmonary disorders, cardiovascular disorders
CC   and renal disorders. The polynucleotide sequences of the invention are
CC   also useful in gene therapy. AAS34767-AAS35050 represent cDNA sequences
CC   encoding for the novel human neoplastic disease associated polypeptides
CC   of the invention.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1269 BP; 362 A; 313 C; 277 G; 312 T; 5 other;

  Query Match             26.5%;  Score 943.2;  DB 22;  Length 1269;
  Best Local Similarity   98.7%;  Pred. No. 7.7e-247;
  Matches  967;  Conservative    3;  Mismatches    8;  Indels    2;  Gaps    2;

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Qy   1968 ccggaggcattcctggaggcagcagatattcctccgagtagccaccccgcagaaggcgtg 2027
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Db    352 ccggaggcattcctggaggcagcagatattcctccgagtagccaccccgcagaaggcgtg 411

Qy   2028 cgattcttccagcagatatgaagattattcagagctgggagagcttcccccacgatctcc 2087
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Db    412 cgattcttccagcagatatgaagattattcagagctgggagagcttcccccacgatctcc 471

Qy   2088 tttagaaccagtttgtgaagatgggccctttggcccccccaccagaggaaaagaaaaggac 2147
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Qy   2148 atctcgtgagctccgagagctgtggcaaaaggctattcttcaacagatactgctgcttag 2207
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Qy   2568 tcctacacacccatacttctctgcccagcttggagcaggacagctatcgctttacaacat 2627
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Db    952 tcctacacacccatacttctctgcccagcttggagcaggacagctatcgctttacaacat 1011

Qy   2628 tttgaaggcctactcacttctagaccaggaagtgggatattgccaaggtctcagctttgt 2687
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Qy   2688 agcaggcattttgcttcttcatatgagtgaggaagaggcgtttaaaatgctcaagtttct 2747
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Qy   2748 gatgtttgacatggggctgcggaaacagtatcggccagacatgattattttacagatcca 2807
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Db   1250 agaacacgaaatcnggccca 1269

RESULT  11
AAH04450
ID   AAH04450 standard; cDNA; 883 BP.
XX
AC   AAH04450;
XX
DT   26-JUN-2001  (first entry)
XX
DE   Human cDNA clone (5'-primer) SEQ ID NO:1285.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
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PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
PS Claim 1; SEQ ID 1285; 2537pp + CD ROM; English.
XX
CC The present invention describes primer sets for synthesising 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.
XX
SQ Sequence 883 BP; 245 A; 221 C; 219 G; 193 T; 5 other;

Query Match 22.1%; Score 785; DB 22; Length 883;
Best Local Similarity 96.7%; Pred. No. 9.9e-204;
Matches 843; Conservative 0; Mismatches 23; Indels 6; Gaps 4;

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Qy   1444 agtgaattaccacccagtgccactcgatttaggctagatatgctgaaaaacaaagcaaag 1503
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 agtgaattaccacccagtgccactcgatttaggctagatatgctgaaaaacaaagcaaag 60

Qy   1504 agatctttaacagagtctttagaaagtattttgtcccggggtaataaagccagaggcctg 1563
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Db     61 agatctttaacagagtctttagaaagtattttgtcccggggtaataaagccagaggcctg 120

Qy   1564 caggaacactccatcagtgtggatctggatagctccctgtctagtacattaagtaacacc 1623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 caggaacactccatcagtgtggatctggatagctccctgtctagtacattaagtaacacc 180

Qy   1624 agcaaagagccatctgtgtgtgaaaaggaggccttgcccatctctgagagctccttttaag 1683
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Db    181 agcaaagagccatctgtgtgtgaaaaggaggccttgcccatctctgagagctccttttaag 240

Qy   1684 ctcctcggctcctcggaggacctgtccagtgactcggagagtcatctcccagaagagcca 1743
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Db    241 ctcctcggctcctcggaggacctgtccagtgactcggagagtcatctcccagaagagcca 300

Qy   1744 gctccgctgtcgccccagcaggccttcaggaggcgagcaaacaccctgagtcacttcccc 1803
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Db    301 gctccgctgtcgccccagcaggccttcaggaggcgagcaaacaccctgagtcacttcccc 360

Qy   1804 atcgaatgccaggaacctccacaacctgcccgggggtccccgggggtttcgcaaaggaaa 1863
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Db    361 atcgaatgccaggaacctccacaacctgcccgggggtccccgggggtttcgcaaaggaaa 420

Qy   1864 cttatgaggtatcactcagtgagcacagagacgcctcatgaacgaaaggactttgaatcc 1923
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 cttatgaggtatcactcagtgagcacagagacgcctcatgaacgaaaggactttgaatcc 480

Qy   1924 aaagcaaaccatcttggtgattctggtgggactcctgtgaagacccggaggcattcctgg 1983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 aaagcaaaccatcttggtgattctggtgggactcctgtgaagacccggaggcattcctgg 540

Qy   1984 aggcagcagatattcctccgagtagccaccccgcagaaggcgtgcgattcttccagcaga 2043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 aggcagcagatattcctccgagtagccaccccgcagaaggcgtgcgattcttccagcaga 600

Qy   2044 tatgaagattattcagagctgggagagcttcccccacgatctcctttagaaccagtttgt 2103
          |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db    601 tatgaagattattcagagctgggagagctt-ccccacgatctcctttagaaccagtttgt 659

Qy   2104 gaagatgggccctttggccccccaccagaggaaaagaaaaggacatctcgtgagctccga 2163
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Db    660 gaagatgggccctttggccccccaccagaggaaaagaaaaggacatctcgtgagctncga 719

Qy   2164 gagc-tgtggcaaaaggctattcttcaacagatactgctgcttagaatggagaaggaaaa 2222
          |||| |||||||||||||||||||||||||||||||| |||||| ||||||||||||||
Db    720 aagcttgtggcaaaaggctattcttcaacagatactgntgcttaaaatggagaaggaaaa 779

Qy   2223 tcagaagctccaagcc---tctgaaaatgatttgctgaacaagcgcc-tgaagctcgatt 2278
          ||||||||| | |  |   |  |||  ||||  |||||||||||| |||| ||||||
Db    780 tcagaagcttccaagccttttgaaaatggattgcttgaacaagcgccttgaacttcgatt 839

Qy   2279 atgaagaaattactccctgtcttaaagaagta 2310
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Db    840 ntgaagaaattactcctggctttaaagaagta 871
```

RESULT 12
AAK92006
ID AAK92006 standard; cDNA; 849 BP.
XX
AC AAK92006;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human cDNA 5'-end sequence, SEQ ID NO: 466.
XX
KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
XX
OS Homo sapiens.
XX
PN EP1130094-A2.
XX
PD 05-SEP-2001.
XX
PF 07-JUL-2000; 2000EP-0114089.
XX
PR 08-JUL-1999; 99JP-0194486.
PR 11-JAN-2000; 2000JP-0118774.
PR 02-MAY-2000; 2000JP-0183765.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
DR WPI; 2001-524255/58.
XX

```
PT   830 Primers useful for synthesizing full length cDNA clones and their
PT   use in genetic manipulation -
XX
PS   Claim 2; SEQ ID NO 466; 1380pp + sequence listing; English.
XX
CC   The invention relates to primers for synthesising full length cDNA
CC   clones. 830 cDNA molecules encoding a human protein have been
CC   isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC   molecules have been determined. Primers for synthesising the full length
CC   cDNA are useful for clarifying the function of the protein encoded by
CC   the cDNA. The full length clones were obtained by construction of full
CC   length enriched cDNA libraries that were synthesised by the oligo-capping
CC   method. The primers enable the production of the full length cDNA easily
CC   without any special methods. The present sequence is the nucleotide
CC   sequence of the 5'-end of a cDNA provided in the invention.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in CD-ROM format directly from EPO.
XX
SQ   Sequence 849 BP; 224 A; 195 C; 196 G; 231 T; 3 other;


  Query Match             16.2%;  Score 574.2;  DB 22;  Length 849;
  Best Local Similarity   98.2%;  Pred. No. 3.5e-146;
  Matches  642;  Conservative    0;  Mismatches    6;  Indels    6;  Gaps    6;

Qy   2555 ttgggcgaacctttcctacacacccatacttctctgcccagcttggagcaggacagctat 2614
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Db    198 tggggcgaacctttcctacacacccatacttctctgcccagcttggagcaggacagctat 257

Qy   2615 cgctttacaacattttgaaggcctactcacttctagaccaggaagtgggatattgccaag 2674
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    258 cgctttacaacattttgaaggcctactcacttctagaccaggaagtgggatattgccaag 317

Qy   2675 gtctcagctttgtagcaggcattttgcttcttcatatgagtgaggaagaggcgtttaaaa 2734
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    318 gtctcagctttgtagcaggcattttgcttcttcatatgagtgaggaagaggcgtttaaaa 377

Qy   2735 tgctcaagtttctgatgtttgacatggggctgcggaaacagtatcggccagacatgatta 2794
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    378 tgctcaagtttctgatgtttgacatggggctgcggaaacagtatcggccagacatgatta 437

Qy   2795 ttttacagatccagatgtaccagctctcgaggttgcttcatgattaccacagagacctct 2854
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    438 ttttacagatccagatgtaccagctctcgaggttgcttcatgattaccacagagacctct 497

Qy   2855 acaatcacctggaggagcacgagatcggccccagcctctacgctgccccctggttcctca 2914
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    498 acaatcacctggaggagcacgagatcggccccagcctctacgctgccccctggttcctca 557

Qy   2915 ccatgtttgcctcacagttcccgctgggattcgtagccagagtctttgatatgatttttc 2974
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    558 ccatgtttgcctcacagttcccgctgggattcgtagccagagtctttgatatgatttttc 617

Qy   2975 ttcagggaacagaggtcatatttaaagtggctttaagtctgttgggaagccataagccct 3034
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    618 ttcagggaacagaggtcatatttaaagtggctttaagtctgttgggaagccataagccct 677

Qy   3035 tgattctgcagcatgaaaacctagaaaccatagttgacttttataaaaagcacgctaccca 3094
           |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db    678 tgattctgcagcatgaaaacctagaaaccatagttgactttataaaaagcacgct-ccca 736

Qy   3095 accttggcttggtacagatggaaaagaccatcaatcaggta-tttgaaatggacatc-gc 3152
           |||||||||||| |||||||||||||||||||||||| ||| |||| |||||||||| |
Db    737 accttggcttgg-acagatggaaaagaccatcaatcangtattttgnaatggacatcggt 795

Qy   3153 taaacagttacaagcttatg-aagttgagtacca-cgtccttcaagaagaactt 3204
           |||||||||||||||||| |||||||| ||| ||||||| ||||||||||
Db    796 taaacagttacaagcttatgaaagttgagtnccaccgtcctttaagaagaactt 849


RESULT  13
AAK93666
ID   AAK93666 standard; cDNA; 849 BP.
XX
AC   AAK93666;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human cDNA clone representative sequence, SEQ ID NO: 2126.
XX
KW   Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
XX
OS   Homo sapiens.
XX
PN   EP1130094-A2.
XX
PD   05-SEP-2001.
XX
PF   07-JUL-2000; 2000EP-0114089.
XX
PR   08-JUL-1999;   99JP-0194486.
PR   11-JAN-2000; 2000JP-0118774.
PR   02-MAY-2000; 2000JP-0183765.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Nishikawa T,  Isogai T,  Hayashi K,  Ishii S,  Kawai Y;
PI   Wakamatsu A,  Sugiyama T,  Nagai K,  Kojima S,  Otsuki T,  Koga H;
XX
DR   WPI; 2001-524255/58.
XX
PT   830 Primers useful for synthesizing full length cDNA clones and their
PT   use in genetic manipulation -
XX
PS   Example 11; SEQ ID NO 2126; 1380pp + sequence listing; English.
XX
CC   The invention relates to primers for synthesising full length cDNA
CC   clones. 830 cDNA molecules encoding a human protein have been
CC   isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC   molecules have been determined. Primers for synthesising the full length
CC   cDNA are useful for clarifying the function of the protein encoded by
CC   the cDNA. The full length clones were obtained by construction of full
CC   length enriched cDNA libraries that were synthesised by the oligo-capping
CC   method. The primers enable the production of the full length cDNA easily
CC   without any special methods. The present sequence was used as the
CC   representative sequence from a human clone which was used in
CC   homology searches to identify the clone.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in CD-ROM format directly from EPO.
XX
SQ   Sequence 849 BP; 224 A; 195 C; 196 G; 231 T; 3 other;


  Query Match             16.2%;  Score 574.2;  DB 22;  Length 849;
  Best Local Similarity   98.2%;  Pred. No. 3.5e-146;
  Matches  642;  Conservative    0;  Mismatches    6;  Indels    6;  Gaps    6;

Qy   2555 ttgggcgaacctttcctacacacccatacttctctgcccagcttggagcaggacagctat 2614
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    198 tggggcgaacctttcctacacacccatacttctctgcccagcttggagcaggacagctat 257

Qy   2615 cgctttacaacattttgaaggcctactcacttctagaccaggaagtgggatattgccaag 2674
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Db    258 cgctttacaacattttgaaggcctactcacttctagaccaggaagtgggatattgccaag 317

Qy   2675 gtctcagctttgtagcaggcattttgcttcttcatatgagtgaggaagaggcgtttaaaa 2734
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    318 gtctcagctttgtagcaggcattttgcttcttcatatgagtgaggaagaggcgtttaaaa 377

Qy   2735 tgctcaagtttctgatgtttgacatggggctgcggaaacagtatcggccagacatgatta 2794
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    378 tgctcaagtttctgatgtttgacatggggctgcggaaacagtatcggccagacatgatta 437

Qy   2795 ttttacagatccagatgtaccagctctcgaggttgcttcatgattaccacagagacctct 2854
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    438 ttttacagatccagatgtaccagctctcgaggttgcttcatgattaccacagagacctct 497
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Qy   2855 acaatcacctggaggagcacgagatcggccccagcctctacgctgccccctggttcctca 2914
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Db    498 acaatcacctggaggagcacgagatcggccccagcctctacgctgccccctggttcctca 557

Qy   2915 ccatgtttgcctcacagttcccgctgggattcgtagccagagtctttgatatgatttttc 2974
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    558 ccatgtttgcctcacagttcccgctgggattcgtagccagagtctttgatatgatttttc 617

Qy   2975 ttcagggaacagaggtcatatttaaagtggctttaagtctgttgggaagccataagccct 3034
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    618 ttcagggaacagaggtcatatttaaagtggctttaagtctgttgggaagccataagccct 677

Qy   3035 tgattctgcagcatgaaaacctagaaaccatagttgactttataaaaagcacgctaccca 3094
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db    678 tgattctgcagcatgaaaacctagaaaccatagttgactttataaaaagcacgct-ccca 736

Qy   3095 accttggcttggtacagatggaaaagaccatcaatcaggta-tttgaaatggacatc-gc 3152
          |||||||||||| |||||||||||||||||||||||| ||| |||| |||||||||| |
Db    737 accttggcttgg-acagatggaaaagaccatcaatcangtattttgnaatggacatcggt 795

Qy   3153 taaacagttacaagcttatg-aagttgagtacca-cgtccttcaagaagaactt 3204
          |||||||||||||||||||| ||||||||| ||| ||||||| ||||||||||
Db    796 taaacagttacaagcttatgaaagttgagtnccaccgtcctttaagaagaactt 849


RESULT 14
AAZ50904
ID   AAZ50904 standard; DNA; 17590 BP.
XX
AC   AAZ50904;
XX
DT   31-MAY-2000  (first entry)
XX
DE   Human TBC-1 partial genomic DNA comprising 5' end sequence.
XX
KW   TBC-1; human; biallelic marker; chromosome 4; cell cycle regulator; SNP;
KW   Single nucleotide polymorphism; tissue differentiation; prostate cancer;
KW   linkage analysis; genetic map; detection; diagnosis; genotyping;
KW   transgenic animal; screening; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_signal      1..2000
FT                    /*tag= a
FT                    /note= "5' Regulatory region"
FT   exon             2001..2077
FT                    /*tag= b
FT                    /number= 1
FT   intron           2078..12739
FT                    /*tag= c
FT                    /number= 1
FT   misc_feature     9391..9845
FT                    /*tag= d
FT                    /note= "Amplicon 99-430"
FT   primer_bind      9391..9408
FT                    /*tag= e
FT                    /bound_moiety= "Primer B1"
FT                    /note= "Amplification of amplicon 99-430"
FT   primer_bind      9475..9493
FT                    /*tag= f
FT                    /bound_moiety= "Primer D1"
FT                    /note= "Microsequencing of marker 99-430-352"
FT   misc_binding     9482..9506
FT                    /*tag= g
FT                    /bound_moiety= "Probe P1"
FT                    /note= "Detection of Biallelic marker 99-430-352"
FT   misc_feature     9494
FT                    /*tag= h
FT                    /note= "Ambiguity base 'R' corresponds to 'A' in allele-1
FT                    and 'G' in allele-2 of biallelic marker 99-430-352"
FT   primer_bind      complement (9495..9513)
FT                    /*tag= i
FT                    /bound_moiety= "Primer E1"
FT                    /note= "Microsequencing of marker 99-430-352"
FT   primer_bind      complement (9828..9845)
FT                    /*tag= j
FT                    /bound_moiety= "Primer C1"
FT                    /note= "Amplification of amplicon 99-430"
FT   exon             12292..12373
FT                    /*tag= k
FT                    /number= 1 bis
FT   intron           12374..12739
FT                    /*tag= l
FT                    /number= 1 bis
FT   exon             12740..13249
FT                    /*tag= m
FT                    /number= 2
FT   intron           13250..17590
FT                    /*tag= n
FT                    /number= 2
XX
PN   WO200008209-A2.
XX
PD   17-FEB-2000.
XX
PF   06-AUG-1999;   99WO-IB01444.
XX
PR   07-AUG-1998;   98US-0095653.
XX
PA   (GEST ) GENSET.
XX
PI   Blumenfeld M,  Bougueleret L,  Chumakov I;
XX
DR   WPI; 2000-205736/18.
XX
PT   New isolated human TBC-1 nucleic acids, useful for developing products
PT   for the diagnosis and treatment of disorders involving cell
PT   proliferation, particularly prostate cancer  -
XX
PS   Claim 1; Page 93-100; 166pp; English.
XX
CC   The present sequence is the partial genomic DNA of human TBC-1 gene,
CC   comprising the 5' regulatory region, exons 1, 1bis and 2. TBC-1 gene is
CC   mapped to a candidate region of prostate cancer on chromosome 4. Single
CC   nucleotide polymorphism (SNP) is located within the biallelic marker
CC   region 99-430-352, localised in intron 1 of TBC-1 genomic DNA.
CC   TBC-1 gene is involved in the regulation of cell cycle and tissue
CC   differentiation in mammals. An alteration of TBC-1 sequence may be
CC   associated with a pathological condition, resulting in abnormal cell
CC   proliferation leading to cancer, e.g. prostate cancer. The biallelic
CC   markers can be used for generation of genetic maps, linkage analysis and
CC   association studies. TBC-1 sequence can be used for detection,
CC   diagnosis, genotyping, production of transgenic animals and screening
CC   of compounds for use in therapy.
XX
SQ   Sequence 17590 BP; 4760 A; 3776 C; 4104 G; 4919 T; 31 other;


  Query Match             11.9%;  Score 422.6;  DB 21;  Length 17590;
  Best Local Similarity   95.8%;  Pred. No. 5.4e-104;
  Matches  434;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

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Db   12833 atggaaccaataacattcacagcaaggaaacatctgctttctaacgaggtctcggtggat 12892

Qy      61 tttggcctgcagctggtgggctccctgcctgtgcattccctgaccaccatgcccatgctg 120
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Db   12893 tttggcctgcagctggtgggctccctgcctgtgcattccctgaccaccatgcccatgctg 12952

Qy     121 ccctgggttgtggctgaggtgcgaagactcagcaggcagtccaccagaaaggaacctgta 180
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Db   12953 ccctgggttgtggctgaggtgcgaagactcagcaggcagtccaccagaaaggaacctgta 13012
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Qy    181 accaagcaagtccggctttgcgtttcaccctctggactgagatgtgaacctgagccaggg 240
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Db  13013 accaagcaagtccggctttgcgtttcaccctctggactgagatgtgaacctgagccaggg 13072

Qy    241 agaagtcaacagtgggatcccctgatctattccagcatctttgagtgcaagcctcagcgt 300
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Db  13073 agaagtcaacagtgggatcccctgatctattccagcatctttgagtgcaagcctcagcgt 13132

Qy    301 gttcacaaactgattcacaacagtcatgacccaagttactttgcttgtctgattaaggaa 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  13133 gttcacaaactgattcacaacagtcatgacccaagttactttgcttgtctgattaaggaa 13192

Qy    361 gacgctgtccaccggcagagtatctgctatgtgttcaaagccgatgatcaaacaaaagtg 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  13193 gacgctgtccaccggcagagtatctgctatgtgttcaaagccgatgatcaaacaaaagta 13252

Qy    421 cctgagatcatcagctccatccgtcaggcgggg 453
          ||||||    | |   |   | ||| | ||
Db  13253 agtgagatggagatccaaaagactaaggtgtgg 13285
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RESULT  15
AAZ15229
ID   AAZ15229 standard; cDNA; 696 BP.
XX
AC   AAZ15229;
XX
DT   12-OCT-1999  (first entry)
XX
DE   Human gene expression product cDNA sequence SEQ ID NO:2698.
XX
KW   Human; gene; gene expression product; diagnosis; therapy; probe;
KW   detection; mapping; tissue typing; profiling; forensic; cancer;
KW   genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9938972-A2.
XX
PD   05-AUG-1999.
XX
PF   28-JAN-1999;   99WO-US01619.
XX
PR   03-APR-1998;   98US-0030666.
PR   28-JAN-1998;   98US-0072910.
PR   24-FEB-1998;   98US-0075954.
PR   31-MAR-1998;   98US-0080114.
PR   03-APR-1998;   98US-0080515.
XX
PA   (CHIR ) CHIRON CORP.
PA   (HYSE-) HYSEQ INC.
XX
PI   Crkvenjakov R,  Dickson M,  Drmanac R,  Drmanac S;
PI   Escobedo J,  Garcia PD,  Garcia V,  Giese K,  Innis MA;
PI   Jones WL,  Kassam A,  Kennedy GC,  Kita D,  Labat I;
PI   Lamson G,  Leshkowitz D,  Pot D,  Randazzo F,  Reinhard C;
PI   Stache-Crain B,  Sudduth-Klinger J,  Williams LT;
XX
DR   WPI; 1999-494092/41.
XX
PT   Novel human genes and their expression products which are
PT   differentially expressed in different cell types
XX
PS   Claim 1; Page 1311; 2479pp; English.
XX
CC   The present invention describes a library of human polynucleotides
CC   comprising the sequences given in AAZ12532 to AAZ17779. Also described is
CC   a method of detecting differentially expressed genes correlated with the
CC   cancerous state of a mammalian cell, comprising detecting at least one
CC   differentially expressed gene product in a test sample from a cell
CC   suspected of being cancerous, where the gene product is encoded by one
CC   of the 5248 polynucleotide sequences given in AAZ12532 to AAZ17779. The
CC   polynucleotides can be used as a source of primers and probes, which can
CC   be used for a variety of purpose, e.g. detection of expression levels,
CC   mapping, tissue typing or profiling, forensics, genetic analysis and
CC   detection of polymorphisms. Polypeptides encoded by the polynucleotides
CC   can be used for raising antibodies for experimental, diagnostic and
CC   therapeutic purposes. The polynucleotides may also be used to construct
CC   arrays for diagnostics (which may be used to determine function of an
CC   encoded protein); and to detect differences in expression levels between
CC   two cells (e.g. to identify abnormal or diseased tissue in a human, to
CC   identify a genetic predisposition or susceptibility to a disease such as
CC   cancer). The polynucleotides of the invention are especially used in the
CC   diagnosis, prognosis and management of colorectal cancer, breast cancer,
CC   and lung cancer. The polynucleotides can also be used to screen for
CC   peptide analogues and antagonists.
XX
SQ   Sequence 696 BP; 189 A; 157 C; 178 G; 142 T; 30 other;
```

```
  Query Match             10.2%;  Score 362;  DB 20;  Length 696;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-88;
  Matches  362;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3194 aagaagaacttatcgattcctctcctctcagtgacaaccaaagaatggataaattagaga 3253
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     59 aagaagaacttatcgattcctctcctctcagtgacaaccaaagaatggataaattagaga 118

Qy   3254 aaaccaacagcagcttacgcaaacagaaccttgacctccttgaacagttgcaggtggcaa 3313
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    119 aaaccaacagcagcttacgcaaacagaaccttgacctccttgaacagttgcaggtggcaa 178

Qy   3314 atggtaggatccaaagccttgaggccaccattgagaagctcctgagcagtgagagcaagc 3373
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Db    179 atggtaggatccaaagccttgaggccaccattgagaagctcctgagcagtgagagcaagc 238

Qy   3374 tgaagcaggccatgcttaccttagaactggagcggtcggccctgctgcagacggtggagg 3433
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    239 tgaagcaggccatgcttaccttagaactggagcggtcggccctgctgcagacggtggagg 298

Qy   3434 agctgcggcggcggagcgcagagcccagcgaccgggagcctgagtgcacgcagcccgagc 3493
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    299 agctgcggcggcggagcgcagagcccagcgaccgggagcctgagtgcacgcagcccgagc 358

Qy   3494 ccacgggcgactgacagctctgcaggagagattgcaacaccatcccacactgtccaggcc 3553
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Db    359 ccacgggcgactgacagctctgcaggagagattgcaacaccatcccacactgtccaggcc 418

Qy   3554 tt 3555
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Db    419 tt 420
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Search completed: September  9, 2002, 19:18:41
Job time: 17499 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: September 9, 2002, 14:24:47 ; Search time 8477.27 Seconds
(without alignments)
8775.683 Million cell updates/sec

Title: US-09-762-311-3_COPY_171_3725
Perfect score: 3555
Sequence: 1 atggaaccaataacattcac.....tcccacactgtccaggcctt 3555

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2751	77.4	3023	9	BC014529	BC014529 Homo sapi
2	2510.4	70.6	4039	6	I86429	I86429 Sequence 1
3	2510.4	70.6	4039	10	MMU33005	U33005 Mus musculu
4	2340	65.8	2576	9	AB029031	AB029031 Homo sapi
5	2112	59.4	2362	9	AK027355	AK027355 Homo sapi
6	1359.2	38.2	1995	4	BTA17923	Y17923 Bos taurus
7	1179.6	33.2	3051	10	BC004675	BC004675 Mus muscu
8	998.4	28.1	1788	9	AK057182	AK057182 Homo sapi
9	682.2	19.2	5922	9	AB011175	AB011175 Homo sapi
c 10	465.8	13.1	189811	30	AC009595	Ac009595 Homo sapi
11	465.8	13.1	195108	9	AC021106	AC021106 Homo sapi
c 12	465.8	13.1	208318	2	AC108933	AC108933 Homo sapi
c 13	424.2	11.9	110000	2	AL390202_04	Continuation (5 of
14	304.6	8.6	3214	3	DMU50542	U50542 Drosophila
15	304.6	8.6	4746	3	DME17919	Y17919 Drosophila
16	284.4	8.0	189811	30	AC009595	Ac009595 Homo sapi
17	284.4	8.0	208318	2	AC108933	AC108933 Homo sapi
18	252.4	7.1	163928	2	AC021335	AC021335 Homo sapi
19	252.4	7.1	180918	9	AC098680	AC098680 Homo sapi
20	245.6	6.9	17019	2	AC019886	AC019886 Drosophil
21	245.6	6.9	161117	3	AC008311	AC008311 Drosophil
22	245.6	6.9	168448	3	AC009346	AC009346 Drosophil
23	245.6	6.9	297832	3	AE003602	AE003602 Drosophil
c 24	180	5.1	163928	2	AC021335	AC021335 Homo sapi
25	141.8	4.0	3761	9	BC014111	BC014111 Homo sapi
c 26	141	4.0	221717	2	AC074357	AC074357 Mus muscu
c 27	139.2	3.9	158310	9	AL162571	AL162571 Human DNA
28	139.2	3.9	183577	2	AC011164	AC011164 Homo sapi
29	132.8	3.7	3691	6	AX078376	AX078376 Sequence
30	132.8	3.7	4560	9	HSA011679	AJ011679 Homo sapi
31	123.8	3.5	154	6	AX261661	AX261661 Sequence
32	119.4	3.4	14119	2	AC013898	AC013898 Drosophil
c 33	119.4	3.4	164413	3	AC023718	AC023718 Drosophil
c 34	119.4	3.4	303648	3	AE003486	AE003486 Drosophil
35	114.6	3.2	2013	9	AF042345	AF042345 Homo sapi
36	114.6	3.2	7383	9	AF008915	AF008915 Homo sapi
c 37	101.8	2.9	30027	3	CELT24D11	U49940 Caenorhabdi
c 38	98	2.8	20553	3	CBRG26M15	AC084540 Caenorhab
c 39	95.6	2.7	73803	8	NCB11B22	AL356834 Neurospor
40	90	2.5	5870	10	MMU53586	U53586 Mus musculu
c 41	84.2	2.4	441	11	G47994	G47994 Z27058_1 Ze
42	80	2.3	27102	3	U41540	U41540 Caenorhabdi
c 43	79.6	2.2	110032	2	AC014916	AC014916 Drosophil
44	79.6	2.2	159660	3	AC010040	AC010040 Drosophil
45	79.6	2.2	282267	3	AE003555	AE003555 Drosophil

ALIGNMENTS

RESULT 1
BC014529
LOCUS BC014529 3023 bp mRNA linear PRI 19-DEC-2001
DEFINITION Homo sapiens, clone IMAGE:3843156, mRNA.
ACCESSION BC014529
VERSION BC014529.1 GI:17939551
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3023)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (24-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 14 Row: c Column: 16
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

FEATURES Location/Qualifiers
source 1. .3023
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3843156"
/tissue_type="Placenta, choriocarcinoma"
/clone_lib="NIH_MGC_21"
/lab_host="DH10B-R"
/note="Vector: pOTB7"

BASE COUNT 883 a 712 c 740 g 688 t
ORIGIN

Query Match 77.4%; Score 2751; DB 9; Length 3023;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2751; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    805 attgagaaccacctcattagcggacacaatattgtgcagcccacagatatcgaggaaaat 864
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     10 ATTGAGAACCACCTCATTAGCGGACACAATATTGTGCAGCCCACAGATATCGAGGAAAAT 69

Qy    865 cgaactatgctcttcacgattggccagtctgaagtttacctcatcagtcctgacaccaaa 924
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     70 CGAACTATGCTCTTCACGATTGGCCAGTCTGAAGTTTACCTCATCAGTCCTGACACCAAA 129

Qy    925 aaaatagcattggagaaaaatttttaaggagatatccttttgctctcagggcatcagacac 984
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    130 AAAATAGCATTGGAGAAAAATTTTAAGGAGATATCCTTTTGCTCTCAGGGCATCAGACAC 189

Qy    985 gtggaccactttgggtttatctgtcgggagtcttccggaggtggcggctttcattttgtc 1044
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    190 GTGGACCACTTTGGGTTTATCTGTCGGGAGTCTTCCGGAGGTGGCGGCTTTCATTTTGTC 249

Qy   1045 tgttacgtgtttcagtgcacaaatgaggctctggttgatgaaattatgatgaccctgaaa 1104
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    250 TGTTACGTGTTTCAGTGCACAAATGAGGCTCTGGTTGATGAAATTATGATGACCCTGAAA 309

Qy   1105 caggccttcacggtggccgcagtgcagcagacagctaaggcgccagcccagctgtgtgag 1164
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Db    310 CAGGCCTTCACGGTGGCCGCAGTGCAGCAGACAGCTAAGGCGCCAGCCCAGCTGTGTGAG 369

Qy   1165 ggctgccccctgcaaagcctgcacaagctctgtgagaggatagagggaatgaattcttcc 1224
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    370 GGCTGCCCCCTGCAAAGCCTGCACAAGCTCTGTGAGAGGATAGAGGGAATGAATTCTTCC 429

Qy   1225 aaaacaaaactagaactgcaaaagcacctgacgacattaaccaatcaggagcaggcgact 1284
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Db    430 AAAACAAAACTAGAACTGCAAAAGCACCTGACGACATTAACCAATCAGGAGCAGGCGACT 489

Qy   1285 atttttgaagaggttcagaaattgagaccgagaaatgagcagcgagagaatgaattgatt 1344
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Db    490 ATTTTTGAAGAGGTTCAGAAATTGAGACCGAGAAATGAGCAGCGAGAGAATGAATTGATT 549

Qy   1345 atttcttttctgagatgtttatatgaagagaaacagaaagaacacatccatattggggag 1404
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1405 atgaagcagacatcgcagatggcagcagagaatattggaagtgaattaccacccagtgcc 1464
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Db    610 ATGAAGCAGACATCGCAGATGGCAGCAGAGAATATTGGAAGTGAATTACCACCCAGTGCC 669

Qy   1465 actcgatttaggctagatatgctgaaaaacaaagcaaagagatctttaacagagtcttta 1524
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Db    670 ACTCGATTTAGGCTAGATATGCTGAAAAACAAAGCAAAGAGATCTTTAACAGAGTCTTTA 729

Qy   1525 gaaagtatttttgtcccggggtaataaagccagaggcctgcaggaacactccatcagtgtg 1584
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    730 GAAAGTATTTTGTCCCGGGGTAATAAAGCCAGAGGCCTGCAGGAACACTCCATCAGTGTG 789

Qy   1585 gatctggatagctccctgtctagtacattaagtaacaccagcaaagagccatctgtgtgt 1644
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1645 gaaaaggaggccttgcccatctctgagagctcctttaagctcctcggctcctcggaggac 1704
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    850 GAAAAGGAGGCCTTGCCCATCTCTGAGAGCTCCTTTAAGCTCCTCGGCTCCTCGGAGGAC 909

Qy   1705 ctgtccagtgactcggagagtcatctcccagaagagccagctccgctgtcgccccagcag 1764
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1765 gccttcaggaggcgagcaaacaccctgagtcacttccccatcgaatgccaggaacctcca 1824
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Qy   1825 caacctgcccgggggtccccgggggtttcgcaaaggaaacttatgaggtatcactcagtg 1884
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1945 tctggtgggactcctgtgaagacccggaggcattcctggaggcagcagatattcctccga 2004
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2005 gtagccaccccgcagaaggcgtgcgattcttccagcagatatgaagattattcagagctg 2064
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Qy   2125 ccaccagaggaaaagaaaaggacatctcgtgagctccgagagctgtggcaaaaggctatt 2184
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Db   1690 CCAAAGGATGTGCCATACAAAGAACTCTTAAAGCAGCTGACTTCCCAGCAGCATGCGATT 1749
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Qy   2725 gcgtttaaaatgctcaagtttctgatgtttgacatggggctgcggaaacagtatcggcca 2784
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Db   1930 GCGTTTAAAATGCTCAAGTTTCTGATGTTTGACATGGGGCTGCGGAAACAGTATCGGCCA 1989

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Qy   3145 gacatcgctaaacagttacaagcttatgaagttgagtaccacgtccttcaagaagaactt 3204
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RESULT   2
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DEFINITION  Sequence 1 from patent US 5700927.
ACCESSION   I86429
VERSION     I86429.1  GI:3206147
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4039)
  AUTHORS   Zon,L. and Richardson,P.
  TITLE     Tbc1 gene and uses thereof
  JOURNAL   Patent: US 5700927-A 1 23-DEC-1997;
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ORIGIN


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Db    592 CGTGTGCACAAACTGATTCACAACAGTCACGACCCGAGCTACTTTGCTTGCCTCATTAAG 651

Qy    358 gaagacgctgtccaccggcagagtatctgctatgtgttcaaagccgatgatcaaacaaaa 417
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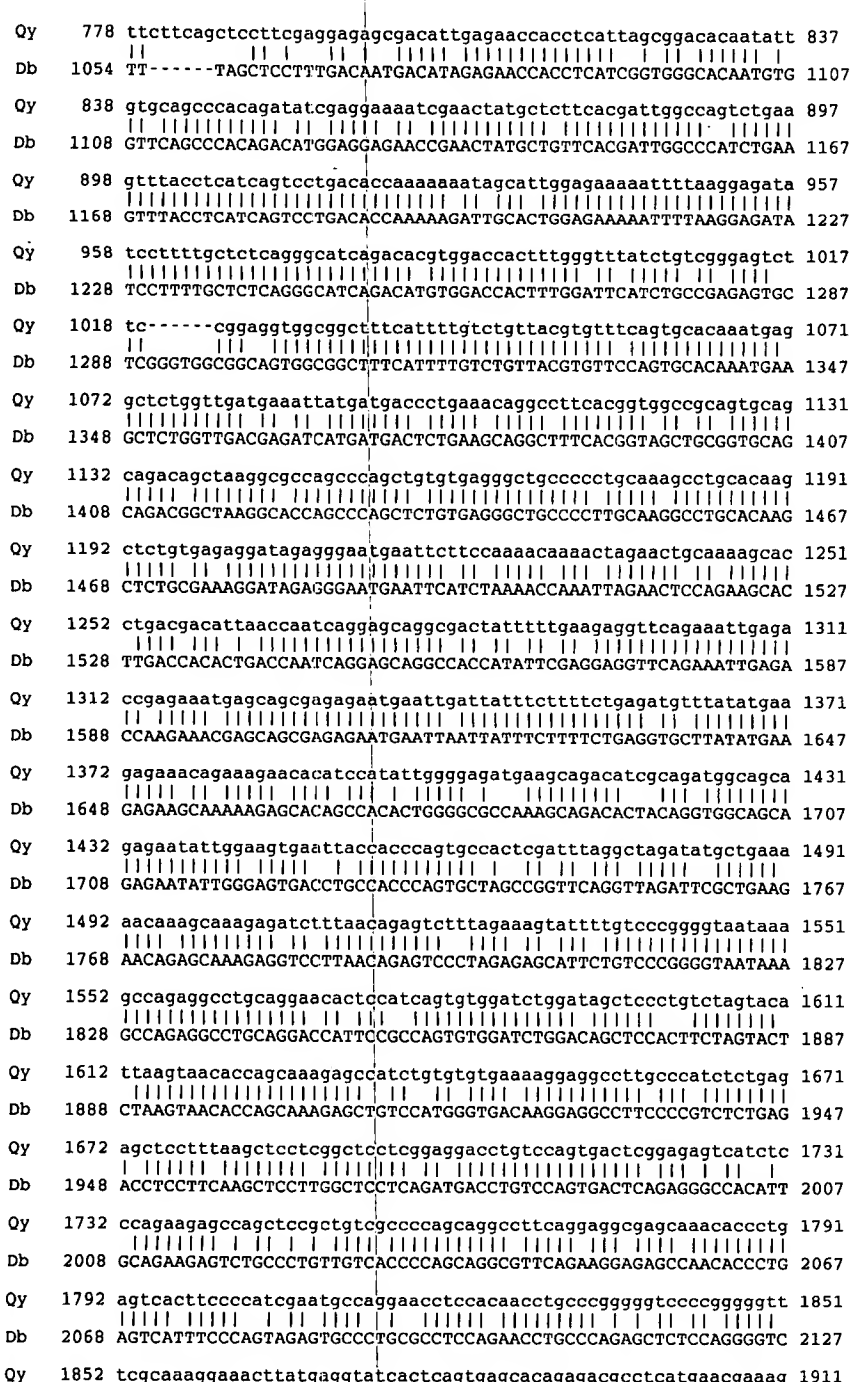
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RESULT   3
MMU33005
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REFERENCE   1  (bases 1 to 4039)
  AUTHORS   Richardson,P.M. and Zon,L.I.
  TITLE     Molecular cloning of a cDNA with a novel domain present in the
            tre-2 oncogene and the yeast cell cycle regulators BUB2 and cdc16
  JOURNAL   Oncogene 11 (6), 1139-1148 (1995)
  MEDLINE   96032578
   PUBMED   7566974
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  AUTHORS   Richardson,P.M. and Zon,L.I.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-1995) Leonard I. Zon, Hematology, Childrens
            Hospital of Boston, HHMI, 300 Longwood Ave., Boston, MA 02115, USA
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ORIGIN


  Query Match           70.6%;  Score 2510.4;  DB 10;  Length 4039;
  Best Local Similarity  83.7%;  Pred. No. 0;
  Matches 2949;  Conservative    0;  Mismatches  536;  Indels   37;  Gaps    8;

Qy      1 atggaaccaataacattcacagcaaggaaacatctgctt-cctaacgaggtctcggtgga 59
          |||||  |||| |||||||||||| |||| |||| | || |||||||| ||||| |||||
Db    292 ATGGAGGCAATCACATTCACAGCGAGGAAGCATCCGTTTCCCTAACGAAGTCTCCGTGGA 351

Qy     60 ttttggcctgcagctggt--gggctccctgcctgtgcattccctgaccaccatgcccatg 117
           || ||| |||||||||||  || |||| | || |||||||| || ||||| |||||||||
Db    352 CTTCGGCTTGCAGCTGGTTGGGTCTCCTTACCCGTGCATTCTCTCACCACTATGCCCATG 411

Qy    118 ctgccctgggttgtggctgaggtgcgaagactcagcaggcagtccaccagaaaggaacct 177
          |||||  ||||| || || ||||| ||||||||||  | |||| | | | |||||| |||
Db    412 CTGCCGTGGGTGGTAGCCGAGGTACGAAGACTCAGTGGCCAGTGCTCTAAAAAGGAGCCT 471

Qy    178 gtaaccaagcaagtccggctttgcgtttcaccctctggactgagatgtgaacctgagcca 237
             || |||||||||| ||||| ||||| ||||| |||||| | || || ||||| |
Db    472 AGGACAAAGCAAGTCCGCCTTTGGGTTTCGCCCTCCGGACTGCGGTGCGAGCCTGACCTG 531

Qy    238 gggagaagtcaacagtgggatcccctgatctattccagcatctttgagtgcaagcctcag 297
          | || |||||||  ||||| || || |||| ||||||||||||||||||||||||||||||
Db    532 GAGAAAAGTCAACCATGGGACCCGCTCATCTGTTCCAGCATCTTTGAGTGCAAGCCTCAG 591

Qy    298 cgtgttcacaaactgattcacaacagtcatgacccaagttactttgcttgtctgattaag 357
          |||||  |||||||||||||||||||||||| ||||| || |||||||||| || ||||||
Db    592 CGTGTGCACAAACTGATTCACAACAGTCACGACCCGAGCTACTTTGCTTGCCTCATTAAG 651

Qy    358 gaagacgctgtccaccggcagagtatctgctatgtgttcaaagccgatgatcaaacaaaa 417
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Db    652 GAGGATGCTGCGCACAGGCAGAGCCTCTGCTATGTGTTTAAAGCAGACGATCAAACAAAA 711

Qy    418 gtgcctgagatcatcagctccatccgtcaggcggggaagatcgcccggcaggaggagctg 477
          ||||||||||||||||||||||||||||| ||||| |||||||| ||||| ||||| ||||||
Db    712 GTGCCTGAGATCATCAGCTCCATCCGGCAGGCCGGGAAGATTGCCCGCCAGGAAGAGCTG 771

Qy    478 cactgcccgtccgagttcgacgacacgttttccaagaagttcgaggtgctcttctgcggc 537
          |  ||||| |||||||||||||| || ||  |||| ||||||||||||||||||||| |||
Db    772 CGTTGCCCCTCCGAGTTCGACGATACCTTCGCCAAAAAGTTCGAGGTGCTCTTCTGTGGC 831

Qy    538 cgcgtgacggtggcgcacaagaaggctccgccggccctgatcgacgagtgcatcgagaag 597
          || ||||| ||||| |||||||||| || || || ||||| |||||||| |||||||||
Db    832 CGGGTGACTGTGGCTCACAAGAAGGCCCCACCCGCACTGATTGACGAGTGTATCGAGAAG 891

Qy    598 ttcaatcacgtcagcggcagccgggggtccgagagcccccgccccaacccgccccatgcc 657
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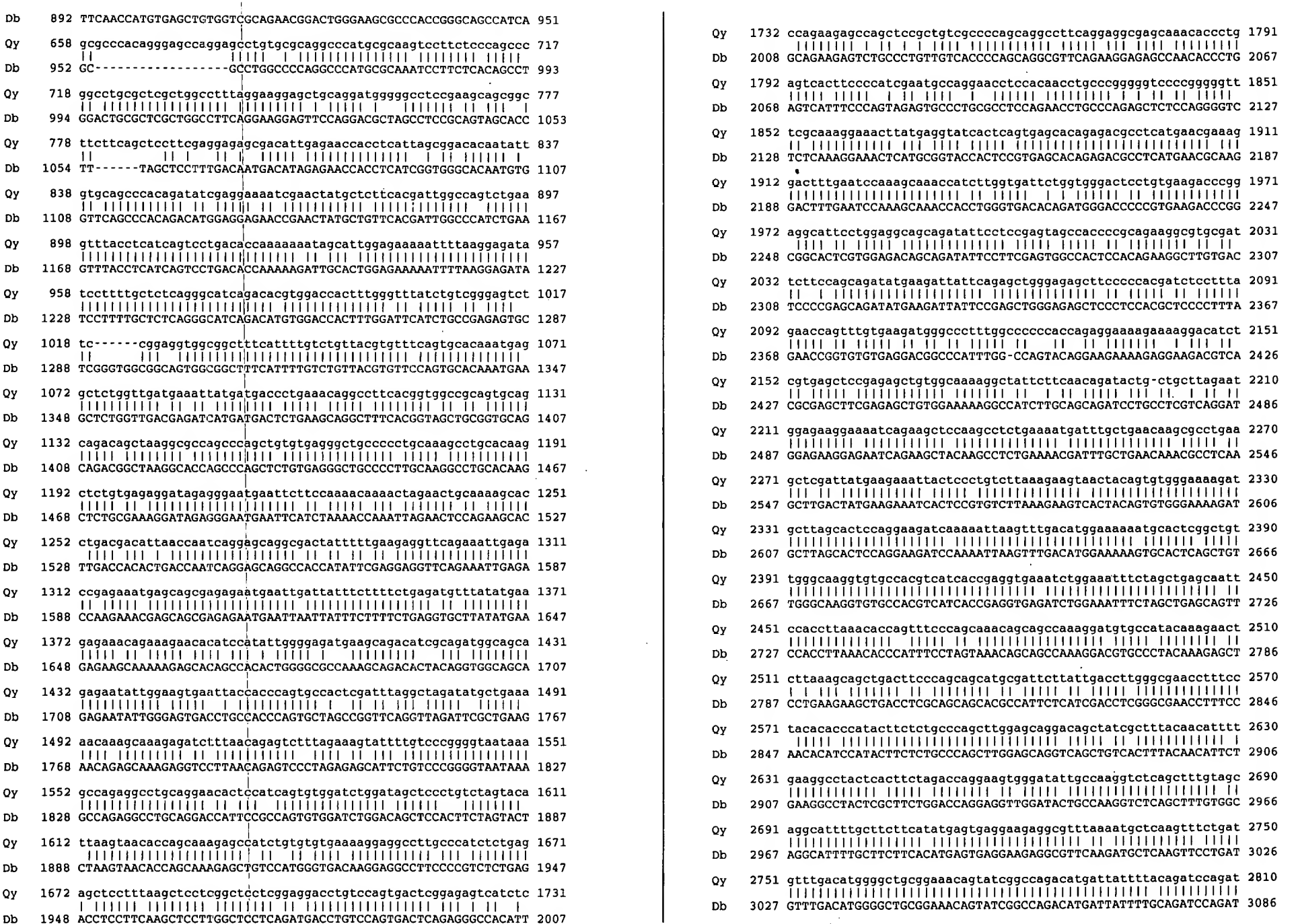

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Db   3087 GTACCAGCTGTCACGGCTCCTCCACGATTACCACCGAGACCTCTACAACCACCTGGAAGA 3146

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Qy   2931 gttcccgctgggattcgtagccagagtctttgatatgatttttcttcagggaacagaggt 2990
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Db   3207 GTTCCCACTCGGCTTTGTAGCCAGAGTCTTTGATATGATCTTCCTTCAGGGATCAGAGGT 3266

Qy   2991 catatttaaagtggctttaagtctgttgggaagccataagcccttgattctgcagcatga 3050
          |||||||||||| |||||||||| ||||| |||||||||||||||||||| ||||||||
Db   3267 CATATTTAAAGTAGCTTTAAGTCTTTTGGGGAGCCATAAGCCCTTGATTCTACAGCATGA 3326

Qy   3051 aaacctagaaaccatagttgactttataaaaagcacgctacccaaccttggcttggtaca 3110
           ||||| |||||||| || ||||| ||||| | ||| || |||||||| ||| |||| ||
Db   3327 GAACCTGGAAACCATCGTGGACTTCATAAAGAACACACTCCCCAACCTGGGCCTGGTGCA 3386

Qy   3111 gatggaaaagaccatcaatcaggtatttgaaatggacatcgctaaacagttacaagctta 3170
          |||||| |||||||||| |||||| |||| |||||||||||| || ||| | || || ||
Db   3387 GATGGAGAAGACCATCAGTCAGGTGTTTGAGATGGACATCGCCAAGCAGCTCCAGGCCTA 3446

Qy   3171 tgaagttgagtaccacgtccttcaagaagaacttatcgattcctctcctctcagtgacaa 3230
          ||| || |||||||||||| | ||| || || ||||| || ||||| ||||||||||||||
Db   3447 TGAGGTCGAGTACCACGTCGTCCAGGAGGAGCTTATTGAGTCCTCGCCTCTCAGTGACAA 3506

Qy   3231 ccaaagaatggataaattagagaaaaccaacagcagcttacgcaaacagaaccttgacct 3290
          |||||||||||| ||||| ||||||||||||||||  || ||||||||||||||||||||
Db   3507 CCAAAGAATGGAGAAATTGGAGAAAACCAACAGCACGTTGCGCAAACAGAACCTTGACCT 3566

Qy   3291 ccttgaacagttgcaggtggcaaatggtaggatccaaagccttgaggccaccattgagaa 3350
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Db   3567 CCTGGAGCAGTTGCAGGTGGCAAATGCTAGGATCCAAAGCCTTGAAGCCACGGTAGAGAA 3626

Qy   3351 gctcctgagcagtgagagcaagctgaagcaggccatgcttaccttagaactggagcggtc 3410
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Db   3627 ACTTCTTACCAGCGAGAGTAAGCTGAAGCAGCGTGCGCTGACCCTGGAGGTGGAGCG--T 3684

Qy   3411 ggccctgctgcagacggtggaggagctgcggcggcggagcgcagagcccagcgaccggga 3470
          |||||||||||| |||||||||||||||| ||| |||||   |||||||   |  ||
Db   3685 CGCCCTGCTGCAGATGGTGGAGGAGCTGCGGAGGCAAAGCGCCCGGCCCAGCACTCCAGA 3744

Qy   3471 gcctgagtgcacgcagcccgagcccacgggcgactgacagct 3512
          ||| || ||||| |||| |||||||| ||||| |||| |||
Db   3745 GCCAGACTGCACCCAGCTGGAGCCCACAGGCGATTGACCGCT 3786


RESULT   4
AB029031
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DEFINITION  Homo sapiens mRNA for KIAA1108 protein, partial cds.
ACCESSION   AB029031
VERSION     AB029031.1  GI:5689552
KEYWORDS    .
SOURCE      Homo sapiens brain cDNA to mRNA, clone_lib:pBluescriptII SK plus
            clone:hh03387.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Kikuno,R., Nagase,T., Ishikawa,K., Hirosawa,M., Miyajima,N.,
            Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.
  TITLE     Prediction of the coding sequences of unidentified human genes.
            XIV. The complete sequences of 100 new cDNA clones from brain which
            code for large proteins in vitro
  JOURNAL   DNA Res. 6 (3), 197-205 (1999)
  MEDLINE   99397452
REFERENCE   2  (bases 1 to 2576)
  AUTHORS   Ohara,O., Nagase,T. and Kikuno,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JUN-1999) Osamu Ohara, Kazusa DNA Research Institute,
            Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba
            292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913,
            Fax:+81-438-52-3914)
FEATURES             Location/Qualifiers
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                     /gene="KIAA1108"
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                     /note="hh03387 cDNA clone for KIAA1108 has a 3306-bp
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                     /translation="NSSKTKLELQKHLTTLTNQEQATIFEEVQKLRPRNEQRENELII
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                     LESILSRGNKARGLQEHSISVDLDSSLSSTLSNTSKEPSVCEKEALPISESSFKLLGS
                     SEDLSSDSESHLPEEPAPLSPQQAFRRRANTLSHFPIECQEPPQPARGSPGVSQRKLM
                     RYHSVSTETPHERKDFESKANHLGDSGGTPVKTRRHSWRQQIFLRVATPQKACDSSSR
                     YEDYSELGELPPRSPLEPVCEDGPFGPPPEEKKRTSRELRELWQKAILQQILLLRMEK
                     ENQKLQASENDLLNKRLKLDYEEITPCLKEVTTVWEKMLSTPGRSKIKFDMEKMHSAV
                     GQGVPRHHRGEIWKFLAEQFHLKHQFPSKQQPKDVPYKELLKQLTSQQHAILIDLGRT
                     FPTHPYFSAQLGAGQLSLYNILKAYSLLDQEVGYCQGLSFVAGILLLHMSEEEAFKML
                     KFLMFDMGLRKQYRPDMIILQIQMYQLSRLLHDYHRDLYNHLEEHEIGPSLYAAPWFL
                     TMFASQFPLGFVARVFDMIFLQGTEVIFKVALSLLGSHKPLILQHENLETIVDFIKST
                     LPNLGLVQMEKTINQVFEMDIAKQLQAYEVEYHVLQEELIDSSPLSDNQRMDKLEKTN
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BASE COUNT      746 a    615 c    628 g    587 t
ORIGIN


  Query Match             65.8%;  Score 2340;  DB 9;  Length 2576;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2340;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1216 aattcttccaaaacaaaactagaactgcaaaagcacctgacgacattaaccaatcaggag 1275
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 AATTCTTCCAAAACAAAACTAGAACTGCAAAAGCACCTGACGACATTAACCAATCAGGAG 60

Qy   1276 caggcgactatttttgaagaggttcagaaattgagaccgagaaatgagcagcgagagaat 1335
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CAGGCGACTATTTTTGAAGAGGTTCAGAAATTGAGACCGAGAAATGAGCAGCGAGAGAAT 120

Qy   1336 gaattgattatttctttttctgagatgtttatatgaagagaaacagaaagaacacatccat 1395
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Db    121 GAATTGATTATTTCTTTTCTGAGATGTTTATATGAAGAGAAACAGAAAGAACACATCCAT 180

Qy   1396 attggggagatgaagcagacatcgcagatggcagcagagaatattggaagtgaattacca 1455
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Db    181 ATTGGGGAGATGAAGCAGACATCGCAGATGGCAGCAGAGAATATTGGAAGTGAATTACCA 240

Qy   1456 cccagtgccactcgatttaggctagatatgctgaaaaacaaagcaaagagatctttaaca 1515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CCCAGTGCCACTCGATTTAGGCTAGATATGCTGAAAAACAAAGCAAAGAGATCTTTAACA 300

Qy   1516 gagtctttagaaagtattttgtcccggggtaataaagccagaggcctgcaggaacactcc 1575
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GAGTCTTTAGAAAGTATTTTGTCCCGGGGTAATAAAGCCAGAGGCCTGCAGGAACACTCC 360

Qy   1576 atcagtgtggatctggatagctccctgtctagtacattaagtaacaccagcaaagagcca 1635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATCAGTGTGGATCTGGATAGCTCCCTGTCTAGTACATTAAGTAACACCAGCAAAGAGCCA 420

Qy   1636 tctgtgtgtgaaaaggaggccttgcccatctctgagagctcctttaagctcctcggctcc 1695
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    421 TCTGTGTGTGAAAAGGAGGCCTTGCCCATCTCTGAGAGCTCCTTTAAGCTCCTCGGCTCC 480

Qy   1696 tcggaggacctgtccagtgactcggagagtcatctcccagaagagccagctccgctgtcg 1755
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TCGGAGGACCTGTCCAGTGACTCGGAGAGTCATCTCCCAGAAGAGCCAGCTCCGCTGTCG 540

Qy   1756 ccccagcaggccttcaggaggcgagcaaacaccctgagtcacttccccatcgaatgccag 1815
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Db    541 CCCCAGCAGGCCTTCAGGAGGCGAGCAAACACCCTGAGTCACTTCCCCATCGAATGCCAG 600

Qy   1816 gaacctccacaacctgcccgggggtccccgggggtttcgcaaaggaaacttatgaggtat 1875
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GAACCTCCACAACCTGCCCGGGGGTCCCCGGGGGTTTCGCAAAGGAAACTTATGAGGTAT 660

Qy   1876 cactcagtgagcacagagacgcctcatgaacgaaaggactttgaatccaaagcaaaccat 1935
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CACTCAGTGAGCACAGAGACGCCTCATGAACGAAAGGACTTTGAATCCAAAGCAAACCAT 720

Qy   1936 cttggtgattctggtgggactcctgtgaagacccggaggcattcctggaggcagcagata 1995
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CTTGGTGATTCTGGTGGGACTCCTGTGAAGACCCGGAGGCATTCCTGGAGGCAGCAGATA 780

Qy   1996 ttcctccgagtagccaccccgcagaaggcgtgcgattcttccagcagatatgaagattat 2055
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TTCCTCCGAGTAGCCACCCCGCAGAAGGCGTGCGATTCTTCCAGCAGATATGAAGATTAT 840

Qy   2056 tcagagctgggagagcttcccccacgatctcctttagaaccagtttgtgaagatgggccc 2115
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TCAGAGCTGGGAGAGCTTCCCCCACGATCTCCTTTAGAACCAGTTTGTGAAGATGGGCCC 900

Qy   2116 tttggcccccccaccagaggaaaagaaaaggacatctcgtgagctccgagagctgtggcaa 2175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 TTTGGCCCCCCACCAGAGGAAAAGAAAAGGACATCTCGTGAGCTCCGAGAGCTGTGGCAA 960

Qy   2176 aaggctattcttcaacagatactgctgcttagaatggagaaggaaaatcagaagctccaa 2235
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 AAGGCTATTCTTCAACAGATACTGCTGCTTAGAATGGAGAAGGAAAATCAGAAGCTCCAA 1020

Qy   2236 gcctctgaaaatgatttgctgaacaagcgcctgaagctcgattatgaagaaattactccc 2295
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GCCTCTGAAAATGATTTGCTGAACAAGCGCCTGAAGCTCGATTATGAAGAAATTACTCCC 1080

Qy   2296 tgtcttaaagaagtaactacagtgtgggaaaagatgcttagcactccaggaagatcaaaa 2355
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Db   1081 TGTCTTAAAGAAGTAACTACAGTGTGGGAAAAGATGCTTAGCACTCCAGGAAGATCAAAA 1140

Qy   2356 attaagtttgacatggaaaaaatgcactcggctgttgggcaaggtgtgccacgtcatcac 2415
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Qy   2416 cgaggtgaaatctggaaatttctagctgagcaattccaccttaaacaccagtttcccagc 2475
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Qy   2656 gaagtgggatattgccaaggtctcagctttgtagcaggcattttgcttcttcatatgagt 2715
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Qy   2776 tatcggccagacatgattattttacagatccagatgtaccagctctcgaggttgcttcat 2835
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Qy   2836 gattaccacagagacctctacaatcacctggaggagcacgagatcggccccagcctctac 2895
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Qy   2896 gctgccccctggttcctcaccatgtttgcctcacagttcccgctgggattcgtagccaga 2955
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Qy   2956 gtctttgatatgatttttcttcagggaacagaggtcatatttaaagtggctttaagtctg 3015
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Qy   3016 ttgggaagccataagcccttgattctgcagcatgaaaacctagaaaccatagttgacttt 3075
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   3076 ataaaaagcacgctacccaaccttggcttggtacagatggaaaagaccatcaatcaggta 3135
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Qy   3196 gaagaacttatcgattcctctcctctcagtgacaaccaaagaatggataaattagagaaa 3255
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Qy   3256 accaacagcagcttacgcaaacagaaccttgacctccttgaacagttgcaggtggcaaat 3315
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Qy   3316 ggtaggatccaaagccttgaggccaccattgagaagctcctgagcagtgagagcaagctg 3375
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Qy   3376 aagcaggccatgcttaccttagaactggagcggtcggccctgctgcagacggtggaggag 3435
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Qy   3436 ctgcggcggcggagcgcagagcccagcgaccgggagcctgagtgcacgcagcccgagccc 3495
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Qy   3496 acgggcgactgacagctctgcaggagagattgcaacaccatcccacactgtccaggcctt 3555
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RESULT   5
AK027355
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DEFINITION  Homo sapiens cDNA FLJ14449 fis, clone HEMBB1001684.
ACCESSION   AK027355
VERSION     AK027355.1  GI:14041975
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens embryo, 10 weeks whole embryo, mainly body cDNA to
            mRNA, clone_lib:HEMBB1 clone:HEMBB1001684.
  ORGANISM  Homo sapiens
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REFERENCE   1  (sites)
  AUTHORS   Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
            Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H.,
            Wagatsuma,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H.,
            Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K.,
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            Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2362)
  AUTHORS   Isogai,T. and Otsuki,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,
            Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology; cDNA library construction,
            5'- & 3'-end one pass sequencing and clone selection: Helix
            Research Institute (supported by Japan Key Technology Center etc.)
            and Department of Virology, Institute of Medical Science,
            University of Tokyo.
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BASE COUNT      657 a    581 c    578 g    546 t
ORIGIN


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Qy   2044 tatgaagattattcagagctgggagagcttcccccacgatctcctttagaaccagtttgt 2103
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REFERENCE   1  (bases 1 to 1995)
  AUTHORS   Xu,X.Z., Wes,P.D., Chen,H., Li,H.S., Yu,M., Morgan,S., Liu,Y. and
            Montell,C.
  TITLE     Retinal targets for calmodulin include proteins implicated in
            synaptic transmission
  JOURNAL   J. Biol. Chem. 273 (47), 31297-31307 (1998)
  MEDLINE   99030403
REFERENCE   2  (bases 1 to 1995)
  AUTHORS   Montell,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-AUG-1998) C. Montell, The Johns Hopkins University
            School of Medicine, Department of Biological Chermistry, 725 N.
            Wolfe Street, Baltimore, MD 21205-2185, USA
FEATURES             Location/Qualifiers
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BASE COUNT      560 a    516 c    497 g    422 t
ORIGIN
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Query Match 38.2%; Score 1359.2; DB 4; Length 1995;
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Matches 1475; Conservative 0; Mismatches 193; Indels 0; Gaps 0;

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Qy   2984 cagaggtcatatttaaagtggctttaagtctgttgggaagccataagcccttgattctgc 3043
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Db   1149 CAGAGGTCATATTTAAAGTGGCTTTAAGTCTGCTGGGAAGCCATAAGCCCTTGATTCTGC 1208

Qy   3044 agcatgaaaacctagaaaccatagttgactttataaaaagcacgctacccaaccttggct 3103
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Qy   3104 tggtacagatggaaaagaccatcaatcaggtatttgaaatggacatcgctaaacagttac 3163
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Qy   3224 gtgacaaccaaagaatggataaattagagaaaaccaacagcagcttacgcaaacagaacc 3283
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Qy   3464 accgggagcctgagtgcacgcagcccgagcccacgggcgactgacagc 3511
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RESULT   7
BC004675
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DEFINITION  Mus musculus, clone IMAGE:3500261, mRNA, partial cds.
ACCESSION   BC004675
VERSION     BC004675.1  GI:14919386
KEYWORDS    .
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 3051)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-MAR-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey Green M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: villalon@bcm.tmc.edu.
            Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
            A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
            Muzny,D.M., Gibbs,R.A.

            Clone distribution: MGC clone distribution information can be found
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            Series: IRAK Plate: 9 Row: m Column: 4.
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                     ELIESSPLSDNQRMEKLEKTNSSLRKQNLDLLEQLQVANARIQSLEATVEKLLTSESK
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ORIGIN
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Qy    2683 tttgtagcaggcattttgcttcttcatatgagtgaggaagaggcgtttaaaatgctcaag 2742

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Qy    3403 gagcggtcggccctgctgcagacggtggaggagctgcggcggcggagcgcagagcccagc 3462

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RESULT 8
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LOCUS AK057182 1788 bp mRNA linear PRI 31-OCT-2001
DEFINITION Homo sapiens cDNA FLJ32620 fis, clone STOMA2000386, highly similar to Bos taurus mRNA for lyncein.
ACCESSION AK057182
VERSION AK057182.1 GI:16552778
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens stomach cDNA to mRNA, clone_lib:STOMA2 clone:STOMA2000386.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Suzuki,O., Sasaki,N., Aotsuka,S., Shoji,T., Ichihara,T., Shiohata,N., Matsumoto,K., Hirano,M., Sano,S., Nomura,R., Yoshikawa,Y., Matsumura,Y., Moriya,S., Chiba,E., Momiyama,H., Onogawa,S., Kaeriyama,S., Satoh,N., Matsunawa,H., Takahashi,E., Kataoka,R., Kuga,N., Kuroda,A., Satoh,I., Kamata,K., Takami,S., Terashima,Y., Watanabe,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1788)
AUTHORS Isogai,T., Otsuki,T. and Sugiyama,T.
TITLE Direct Submission
JOURNAL Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952)
COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and HRI.
FEATURES Location/Qualifiers
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Qy   2736 gctcaagtttctgatgtttgacatggggctgcggaaacagtatcggccagacatgattat 2795
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Qy   2796 tttacagatccagatgtaccagctctcgaggttgcttcatgattaccacagagacctcta 2855
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Qy   2916 catgtttgcctcacagttcccgctgggattcgtagccagagtctttgatatgatttttct 2975
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RESULT   9
AB011175
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DEFINITION  Homo sapiens mRNA for KIAA0603 protein, complete cds.
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VERSION     AB011175.1  GI:3043729
KEYWORDS    KIAA0603 protein.
SOURCE      Homo sapiens male brain cDNA to mRNA, clone_lib:pBluescriptII SK
            plus clone:HG1488b.
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 5922)
  AUTHORS   Ohara,O., Nagase,T. and Ishikawa,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-FEB-1998) Osamu Ohara, Kazusa DNA Research Institute,
            DNA Technology; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913,
            Fax:+81-438-52-3914)
REFERENCE   2  (sites)
  AUTHORS   Nagase,T., Ishikawa,K., Miyajima,N., Tanaka,A., Kotani,H.,
            Nomura,N. and Ohara,O.
  TITLE     Prediction of the coding sequences of unidentified human genes. IX.
            The complete sequences of 100 new cDNA clones from brain which can
            code for large proteins in vitro
  JOURNAL   DNA Res. 5 (1), 31-39 (1998)
  MEDLINE   98290545
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                     MLKFLMYDLGFRKQYRPDMMSLQIQMYQLSRLLHDYHRDLYNHLEENEISPSLYAAPW
                     FLTLFASQFSLGFVARVFDIIFLQGTEVIFKVALSLLSSQETLIMECESFENIVEFLK
                     NTLPDMNTSEMEKIITQVFEMDISKQLHAYEVEYHVLQDELQESSYSCEDSETLEKLE
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BASE COUNT     1624 a   1408 c   1432 g   1458 t
ORIGIN
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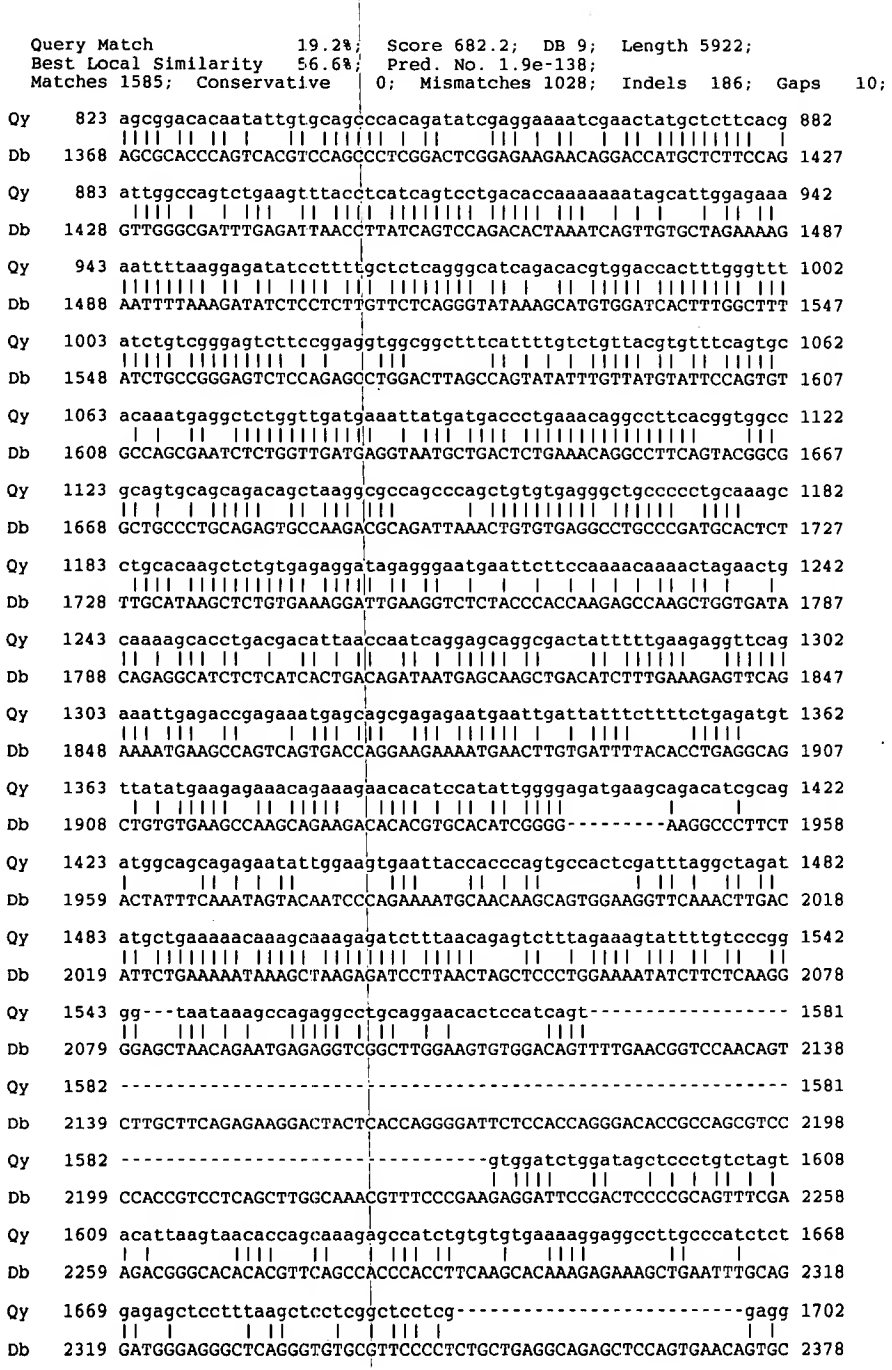
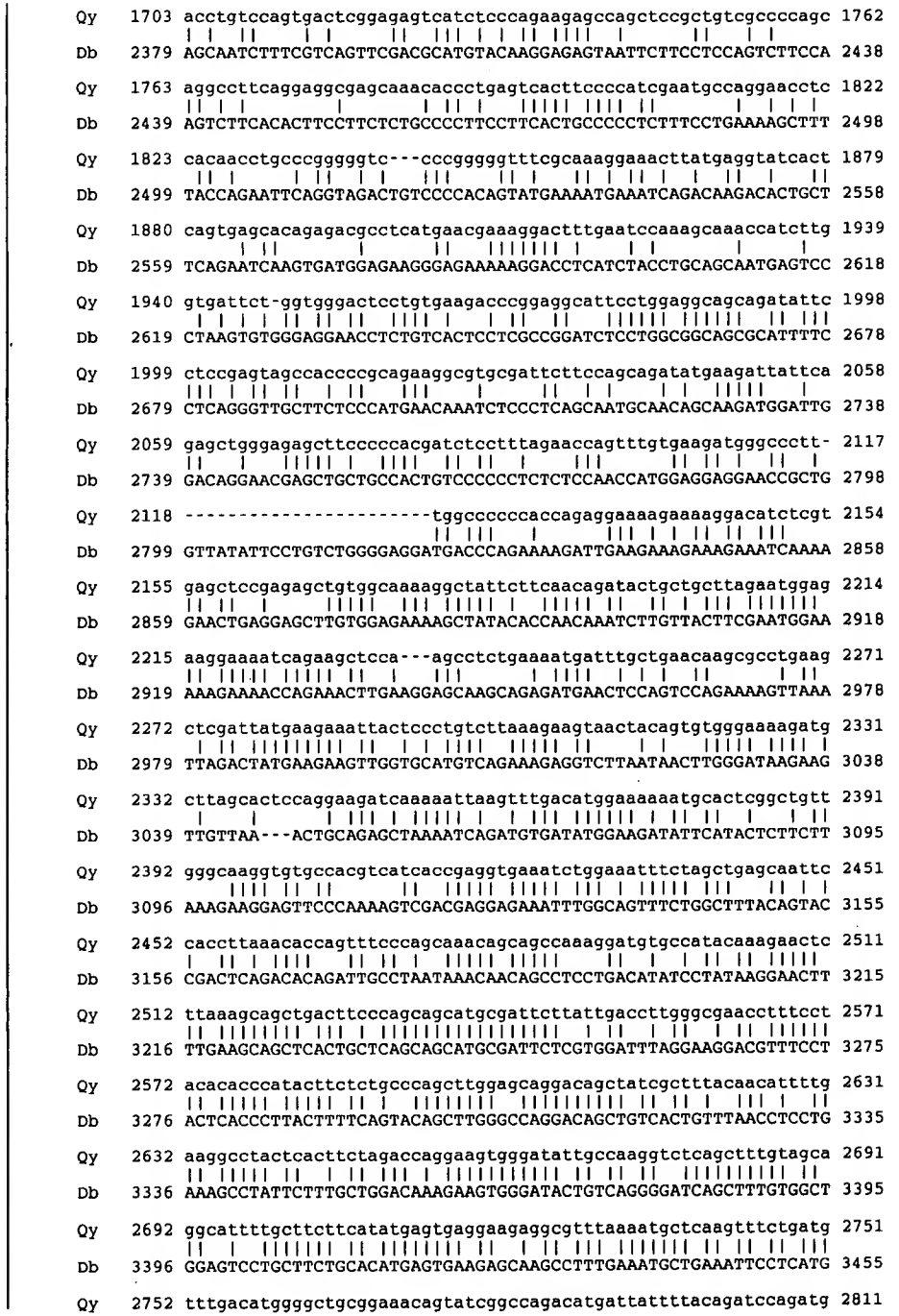
Query Match 19.2%; Score 682.2; DB 9; Length 5922;
Best Local Similarity 56.6%; Pred. No. 1.9e-138;
Matches 1585; Conservative 0; Mismatches 1028; Indels 186; Gaps 10;





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Qy    2812 taccagctctcgaggttgcttcatgattaccacagagacctctacaatcacctggaggag 2871

Db    3516 TACCAGCTGTCCAGGCTCCTTCATGACTATCACAGAGATCTCTACAATCACCTTGAAGAA 3575

Qy    2872 cacgagatcggccccagcctctacgctgccccctggttcctcaccatgtttgcctcacag 2931

Db    3576 AATGAAATCAGCCCCAGTCTTTATGCTGCCCCCTGGTTCCTCACATTGTTTGCCTCTCAG 3635

Qy    2932 ttcccgctgggattcgtagccagagtctttgatatgatttttcttcagggaacagaggtc 2991

Db    3636 TTTTCATTAGGATTTGTAGCCAGAGTTTTTGATATTATTTTTCTTCAGGGAACTGAAGTT 3695

Qy    2992 atatttaaagtggctttaagtctgttgggaagccataagcccttgattctgcagcatgaa 3051

Db    3696 ATATTCAAGGTTGCACTCAGCCTACTGAGCAGCCAAGAGACACTTATAATGGAATGTGAG 3755

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Db    3756 AGCTTTGAAAATATTGTTGAGTTTCTTAAAAACACGCTACCTGATATGAATACCTCTGAA 3815

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Db    3816 ATGGAAAAAATTATTACCCAGGTTTTTGAGATGGATATTTCTAAGCAGTTGCATGCCTAT 3875

Qy    3172 gaagttgagtaccacgtccttcaagaagaacttatcgattcctctcctctcagt---gac 3228

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Qy    3229 aaccaaagaatggataaattagagaaaaccaacagcagcttacgcaaacagaaccttgac 3288

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Qy    3289 ctccttgaacagttgcaggtggcaaatggtaggatccaaagccttgaggccaccattgag 3348

Db    3996 CTCCTAGAAAAATTACAGGTAGCTCATACTAAAATCCAGGCCTTGGAATCAAACCTGGAA 4055

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Db    4056 AATCTTTTGACGAGAGAGACCAAAATGAAGTCTTTAATCCGGACCCTGGAACAAGAAAAA 4115

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Db    4116 ATGGCTTATCAAAAGACAGTGGAGCAACTCCGGAAGCTG 4154


RESULT 10
AC009595/c
ID   AC009595   standard; DNA; HTG; 189811 BP.
XX
AC   AC009595;
XX
SV   AC009595.3
XX
DT   30-AUG-1999 (Rel. 60, Created)
DT   03-JUL-2000 (Rel. 64, Last updated, Version 4)
XX
DE   Homo sapiens chromosome 4 clone RP11-392K14 map 4, WORKING DRAFT SEQUENCE,
DE   28 unordered pieces.
XX
KW   HTG; HTGS_DRAFT; HTGS_PHASE1.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
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RN   [1]
RP   1-189811
RA   Birren B., Linton L., Nusbaum C., Lander E.;
RT   "Homo sapiens chromosome 4, clone RP11-392K14";
RL   Unpublished.
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RN   [2]
RP   1-189811
RA   Birren B., Linton L., Nusbaum C., Lander E., Allen N., Anderson M.,
RA   Baker J., Baldwin J., Barna N., Beckerly R., Benn J., Brown A., Castle A.,
RA   Cerny J., Colangelo M., Collins S., Collymore A., Cooke P., DeArellano K.,
RA   Depayre E., Devon K., Dewar K., Donelan L., Doyle M., Ferreira P.,
RA   FitzHugh W., Forrest C., Funke R., Gage D., Galagan J., Gardyna S.,
RA   Gilbert D., Grant G., Hagos B., Heaford A., Horton L., Howland J.C.,
RA   Jones C., Kann L., Karatas A., Lehoczky J., Lieu C., Locke K.,
RA   Macdonald P., Marquis N., McEwan P., McGurk A., McKernan K., McLaughlin J.,
RA   Meldrim J., Molla M., Morris W., Morrow J., Mychaleckyj J., Naylor J.,
RA   Niloff M., O'Connor T., O'Donnell P., Pavlin B., Peterson K., Pollara V.,
RA   Riley R., Roberts D., Roy A., Severy P., Stange-Thomann N., Stojanovic N.,
RA   Stone C., Subramanian A., Tesfaye S., Torruella-Miller I., Vassiliev H.,
RA   Vo A., Wagner A., Wheeler J., Wu X., Wyman D., Ye W.J., Zody M.;
RT   ;
RL   Submitted (27-AUG-1999) to the EMBL/GenBank/DDBJ databases.
RL   Whitehead Institute/MIT Center for Genome Research, 320 Charles Street,
RL   Cambridge, MA 02141, USA
XX
CC   On Jun 23, 2000 this sequence version replaced gi:6006228.
CC   All repeats were identified using RepeatMasker:
CC   Smit, A.F.A. & Green, P. (1996-1997)
CC   http://ftp.genome.washington.edu/RM/RepeatMasker.html
CC   -------------- Genome Center
CC   Center: Whitehead Institute/ MIT Center for Genome Research
CC   Center code: WIBR
CC   Web site: http://www-seq.wi.mit.edu
CC   Contact: sequence_submissions@genome.wi.mit.edu
CC   -------------- Project Information
CC   Center project name: L1755
CC   Center clone name: 392_K_14
CC   -------------- Summary Statistics
CC   Sequencing vector: M13; M77815; 100% of reads
CC   Chemistry: Dye-primer-amersham; 5% of reads
CC   Chemistry: Dye-terminator Big Dye; 95% of reads
CC   Assembly program: Phrap; version 0.960731
CC   Consensus quality: 164704 bases at least Q40
CC   Consensus quality: 175594 bases at least Q30
CC   Consensus quality: 181024 bases at least Q20
CC   Insert size: 214000; agarose-fp
CC   Insert size: 187111; sum-of-contigs
CC   Quality coverage: 3.0 in Q20 bases; agarose-fp
CC   Quality coverage: 3.5 in Q20 bas.
CC   * NOTE: This is a 'working draft' sequence. It currently
CC   * consists of 28 contigs. The true order of the pieces
CC   * is not known and their order in this sequence record is
CC   * arbitrary. Gaps between the contigs are represented as
CC   * runs of N, but the exact sizes of the gaps are unknown.
CC   * This record will be updated with the finished sequence
CC   * as soon as it is available and the accession number will
CC   * be preserved.
CC   *        1      451: contig of 451 bp in length
CC   *      452 551: gap of      100 bp
CC   *      552     2663: contig of 2112 bp in length
CC   *     2664 2763: gap of      100 bp
CC   *     2764     4124: contig of 1361 bp in length
CC   *     4125 4224: gap of      100 bp
CC   *     4225     6767: contig of 2543 bp in length
CC   *     6768 6867: gap of      100 bp
CC   *     6868     8750: contig of 1883 bp in length
CC   *     8751 8850: gap of      100 bp
CC   *     8851    11272: contig of 2422 bp in length
CC   *    11273 11372: gap of      100 bp
CC   *    11373    13411: contig of 2039 bp in length
CC   *    13412 13511: gap of      100 bp
CC   *    13512    16962: contig of 3451 bp in length
CC   *    16963 17062: gap of      100 bp
CC   *    17063    22544: contig of 5482 bp in length
CC   *    22545 22644: gap of      100 bp
CC   *    22645    26284: contig of 3640 bp in length
CC   *    26285 26384: gap of      100 bp
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CC   *    31224 31323: gap of    100 bp
CC   *    31324    36014: contig of 4691 bp in length
CC   *    36015 36114: gap of    100 bp
CC   *    36115    41939: contig of 5825 bp in length
CC   *    41940 42039: gap of    100 bp
CC   *    42040    48122: contig of 6083 bp in length
CC   *    48123 48222: gap of    100 bp
CC   *    48223    52983: contig of 4761 bp in length
CC   *    52984 53083: gap of    100 bp
CC   *    53084    58094: contig of 5011 bp in length
CC   *    58095 58194: gap of    100 bp
CC   *    58195    64606: contig of 6412 bp in length
CC   *    64607 64706: gap of    100 bp
CC   *    64707    71079: contig of 6373 bp in length
CC   *    71080 71179: gap of    100 bp
CC   *    71180    79886: contig of 8707 bp in length
CC   *    79887 79986: gap of    100 bp
CC   *    79987    86155: contig of 6169 bp in length
CC   *    86156 86255: gap of    100 bp
CC   *    86256    95370: contig of 9115 bp in length
CC   *    95371 95470: gap of    100 bp
CC   *    95471   103712: contig of 8242 bp in length
CC   *   103713 103812: gap of    100 bp
CC   *   103813   113565: contig of 9753 bp in length
CC   *   113566 113665: gap of    100 bp
CC   *   113666   123867: contig of 10202 bp in length
CC   *   123868 123967: gap of    100 bp
CC   *   123968   132296: contig of 8329 bp in length
CC   *   132297 132396: gap of    100 bp
CC   *   132397   141110: contig of 8714 bp in length
CC   *   141111 141210: gap of    100 bp
CC   *   141211   161622: contig of 20412 bp in length
CC   *   161623 161722: gap of    100 bp
CC   *   161723   189811: contig of 28089 bp in length.
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FT                   /map="4"
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FT   misc_feature    552. .2663
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FT   misc_feature    6868. .8750
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FT   misc_feature    11373. .13411
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FT   misc_feature    13512. .16962
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FT   misc_feature    17063. .22544
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FT   misc_feature    22645. .26284
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FT   misc_feature    95471. .103712
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FT   misc_feature    103813. .113565
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FT                   /note="assembly_fragment"
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SQ   Sequence 189811 BP; 52455 A; 40839 C; 40321 G; 53485 T; 2711 other;


  Query Match             13.1%;  Score 465.8;  DB 30;  Length 189811;
  Best Local Similarity   99.6%;  Pred. No. 5.2e-91;
  Matches  467;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy     416 aagtgcctgagatcatcagctccatccgtcaggcggggaagatcgcccggcaggaggagc 475
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   97313 AGGTGCCTGAGATCATCAGCTCCATCCGTCAGGCGGGGAAGATCGCCCGGCAGGAGGAGC 97254

Qy     476 tgcactgcccgtccgagttcgacgacacgttttccaagaagttcgaggtgctcttctgcg 535
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   97253 TGCACTGCCCGTCCGAGTTCGACGACACGTTTTCCAAGAAGTTCGAGGTGCTCTTCTGCG 97194

Qy     536 gccgcgtgacggtggcgcacaagaaggctccgccggccctgatcgacgagtgcatcgaga 595
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   97193 GCCGCGTGACGGTGGCGCACAAGAAGGCTCCGCCGGCCCTGATCGACGAGTGCATCGAGA 97134

Qy     596 agttcaatcacgtcagcggcagccgggggtccgagagcccccgccccaaccccgccccatg 655
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   97133 AGTTCAATCACGTCAGCGGCAGCCGGGGGTCCGAGAGCCCCCGCCCCAACCCGCCCCATG 97074

Qy     656 ccgcgcccacagggagccaggagcctgtgcgcaggcccatgcgcaagtccttctcccagc 715
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   97073 CCGCGCCCACAGGGAGCCAGGAGCCTGTGCGCAGGCCCATGCGCAAGTCCTTCTCCCAGC 97014

Qy     716 ccggcctgcgctcgctggcctttaggaaggagctgcaggatgggggcctccgaagcagcg 775
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   97013 CCGGCCTGCGCTCGCTGGCCTTTAGGAAGGAGCTGCAGGATGGGGGCCTCCGAAGCAGCG 96954

Qy     776 gcttcttcagctccttcgaggagagcgacattgagaaccacctcattagcggacacaata 835
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Db   96953 GCTTCTTCAGCTCCTTCGAGGAGAGCGACATTGAGAACCACCTCATTAGCGGACACAATA 96894

Qy     836 ttgtgcagcccacagatatcgaggaaaatcgaactatgctcttcacgat 884
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Db   96893 TTGTGCAGCCCACAGATATCGAGGAAAATCGAACTATGCTCTTCACGGT 96845


RESULT  11
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LOCUS       AC021106              195108 bp    DNA     linear   PRI 03-JUL-2001
DEFINITION  Homo sapiens clone RP11-177C12, complete sequence.
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ACCESSION   AC021106
VERSION     AC021106.6  GI:14589687
KEYWORDS    HTG.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 195108)
  AUTHORS   Waterston,R.H.
  TITLE     The sequence of Homo sapiens clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 195108)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-JAN-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   3  (bases 1 to 195108)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-JUL-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
COMMENT     On Jul 3, 2001 this sequence version replaced gi:14018126.

            ------------------- Genome Center --------------------
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site:http://genome.wustl.edu/gsc/index.shtml
            ---------------- Project Information -----------------
            Center project name: H_NH0177C12
            ------------------------------------------------------.
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BASE COUNT    53372 a  40112 c  41873 g  59751 t
ORIGIN


  Query Match             13.1%;  Score 465.8;  DB 9;  Length 195108;
  Best Local Similarity   99.6%;  Pred. No. 5.2e-91;
  Matches  467;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    416 aagtgcctgagatcatcagctccatccgtcaggcggggaagatcgcccggcaggaggagc 475
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Qy    476 tgcactgcccgtccgagttcgacgacacgttttccaagaagttcgaggtgctcttctgcg 535
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Db 180819 TGCACTGCCCGTCCGAGTTCGACGACACGTTTTCCAAGAAGTTCGAGGTGCTCTTCTGCG 180878

Qy    536 gccgcgtgacggtggcgcacaagaaggctccgccggccctgatcgacgagtgcatcgaga 595
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Db 180879 GCCGCGTGACGGTGGCGCACAAGAAGGCTCCGCCGGCCCTGATCGACGAGTGCATCGAGA 180938

Qy    596 agttcaatcacgtcagcggcagccgggggtccgagagcccccgccccaacccgccccatg 655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 180939 AGTTCAATCACGTCAGCGGCAGCCGGGGGTCCGAGAGCCCCCGCCCCAACCCGCCCCATG 180998

Qy    656 ccgcgcccacagggagccaggagcctgtgcgcaggcccatgcgcaagtccttctcccagc 715
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Db 180999 CCGCGCCCACAGGGAGCCAGGAGCCTGTGCGCAGGCCCATGCGCAAGTCCTTCTCCCAGC 181058

Qy    716 ccggcctgcgctcgctggcctttaggaaggagctgcaggatgggggcctccgaagcagcg 775
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Qy    776 gcttcttcagctccttcgaggagagcgacattgagaaccacctcattagcggacacaata 835
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Qy    836 ttgtgcagcccacagatatcgaggaaaatcgaactatgctcttcacgat 884
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RESULT  12
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DEFINITION  Homo sapiens chromosome 4 clone RP11-392K14, WORKING DRAFT
            SEQUENCE, 5 unordered pieces.
ACCESSION   AC108933 AC009595
VERSION     AC108933.1  GI:18464316
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 208318)
  AUTHORS   Waterston,R.H.
  TITLE     The sequence of Homo sapiens clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 208318)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-FEB-2002) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
COMMENT     On Feb 1, 2002 this sequence version replaced gi:8671945.

            ------------------- Genome Center --------------------
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site:http://genome.wustl.edu/gsc/index.shtml
            Contact: submissions@watson.wustl.edu
            ---------------- Project Information -----------------
            Center project name: H_NH0392K14
            Drafting center: WIBR
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            -------------- Summary Statistics  --------------
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            Sequencing vector: plasmid; %
            Chemistry: Dye-primer ET; % of reads
            Chemistry: Dye-terminator Big Dye; % of reads
            Assembly program: Phrap; version 0.990319
            Consensus quality: 205652 bases at least Q40
            Consensus quality: 206608 bases at least Q30
            Consensus quality: 207022 bases at least Q20
            Insert size: 218000; agarose-fp
            Insert size: 207918; sum-of-contigs
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            Quality coverage: 6.62 in Q20 bases; sum-of-contigs
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            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 5 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
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            *    65132    65231: gap of unknown length
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            *   105029   105128: gap of unknown length
            *   105129   159307: contig of 54179 bp in length
            *   159308   159407: gap of unknown length
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                     /db_xref="taxon:9606"
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     misc_feature    105129. .159307
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ORIGIN


  Query Match             13.1%;  Score 465.8;  DB 2;  Length 208318;
  Best Local Similarity   99.6%;  Pred. No. 5.2e-91;
  Matches  467;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    416 aagtgcctgagatcatcagctccatccgtcaggcggggaagatcgcccggcaggaggagc 475
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 129553 AGGTGCCTGAGATCATCAGCTCCATCCGTCAGGCGGGGAAGATCGCCCGGCAGGAGGAGC 129494

Qy    476 tgcactgcccgtccgagttcgacgacacgttttccaagaagttcgaggtgctcttctgcg 535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 129493 TGCACTGCCCGTCCGAGTTCGACGACACGTTTTCCAAGAAGTTCGAGGTGCTCTTCTGCG 129434

Qy    536 gccgcgtgacggtggcgcacaagaaggctccgccggccctgatcgacgagtgcatcgaga 595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 129433 GCCGCGTGACGGTGGCGCACAAGAAGGCTCCGCCGGCCCTGATCGACGAGTGCATCGAGA 129374

Qy    596 agttcaatcacgtcagcggcagccgggggtccgagagcccccgccccaacccgccccatg 655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 129373 AGTTCAATCACGTCAGCGGCAGCCGGGGGTCCGAGAGCCCCCGCCCCAACCCGCCCCATG 129314

Qy    656 ccgcgcccacagggagccaggagcctgtgcgcaggcccatgcgcaagtccttctcccagc 715
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 129313 CCGCGCCCACAGGGAGCCAGGAGCCTGTGCGCAGGCCCATGCGCAAGTCCTTCTCCCAGC 129254

Qy    716 ccggcctgcgctcgctggcctttaggaaggagctgcaggatgggggcctccgaagcagcg 775
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 129253 CCGGCCTGCGCTCGCTGGCCTTTAGGAAGGAGCTGCAGGATGGGGGCCTCCGAAGCAGCG 129194

Qy    776 gcttcttcagctccttcgaggagagcgacattgagaaccacctcattagcggacacaata 835
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 129193 GCTTCTTCAGCTCCTTCGAGGAGAGCGACATTGAGAACCACCTCATTAGCGGACACAATA 129134

Qy    836 ttgtgcagcccacagatatcgaggaaaatcgaactatgctcttcacgat 884
          |||||||||||||||||||||||||||||||||||||||||||||||| |
Db 129133 TTGTGCAGCCCACAGATATCGAGGAAAATCGAACTATGCTCTTCACGGT 129085


RESULT  13
AL390202_04/c
WPCOMMENT
  Sequence split into 10 fragments  LOCUS AL390202 Accession AL390202
     Fragment Name      Begin    End
     AL390202_00            1    110000
     AL390202_01       100001    210000
     AL390202_02       200001    310000
     AL390202_03       300001    410000
     AL390202_04       400001    510000
     AL390202_05       500001    610000
     AL390202_06       600001    710000
     AL390202_07       700001    810000
     AL390202_08       800001    910000
     AL390202_09       900001    988176
Continuation (5 of 10) of AL390202 from base 400001 (AL390202 Homo sapiens chromosome 20


  Query Match             11.9%;  Score 424.2;  DB 2;  Length 110000;
  Best Local Similarity   96.0%;  Pred. No. 6.1e-82;
  Matches  435;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy      1 atggaaccaataacattcacagcaaggaaacatctgcttcctaacgaggtctcggtggat 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10365 ATGGAACCAATAACATTCACAGCAAGGAAACATCTGCTTCCTAACGAGGTCTCGGTGGAT 10306

Qy     61 tttggcctgcagctggtgggctccctgcctgtgcattccctgaccaccatgcccatgctg 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10305 TTTGGCCTGCAGCTGGTGGGCTCCCTGCCTGTGCATTCCCTGACCACCATGCCCATGCTG 10246

Qy    121 ccctgggttgtggctgaggtgcgaagactcagcaggcagtccaccagaaaggaacctgta 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10245 CCCTGGGTTGTGGCTGAGGTGCGAAGACTCAGCAGGCAGTCCACCAGAAAGGAACCTGTA 10186

Qy    181 accaagcaagtccggctttgcgtttcaccctctggactgagatgtgaacctgagccaggg 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10185 ACCAAGCAAGTCCGGCTTTGCGTTTCACCCTCTGGACTGAGATGTGAACCTGAGCCAGGG 10126

Qy    241 agaagtcaacagtgggatcccctgatctattccagcatctttgagtgcaagcctcagcgt 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10125 AGAAGTCAACAGTGGGATCCCCTGATCTATTCCAGCATCTTTGAGTGCAAGCCTCAGCGT 10066

Qy    301 gttcacaaactgattcacaacagtcatgacccaagttacttttgcttgtctgattaaggaa 360
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Db  10065 GTTCACAAACTGATTCACAACAGTCATGACCCAAGTTACTTTGCTTGTCTGATTAAGGAA 10006

Qy    361 gacgctgtccaccggcagagtatctgctatgtgttcaaagccgatgatcaaacaaaagtg 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10005 GACGCTGTCCACCGGCAGAGTATCTGCTATGTGTTCAAAGCCGATGATCAAACAAAAGTA 9946

Qy    421 cctgagatcatcagctccatccgtcaggcgggg 453
          ||||||    | |   |    | ||| | ||
Db   9945 AGTGAGATGGAGATCCAAAAGACTAAGGTGTGG 9913


RESULT  14
DMU50542
LOCUS       DMU50542                3214 bp    mRNA    linear   INV 12-JUN-1996
DEFINITION  Drosophila melanogaster pollux (plx) mRNA, complete cds.
ACCESSION   U50542
VERSION     U50542.1  GI:1373162
KEYWORDS    .
SOURCE      fruit fly strain=Oregon R.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 3214)
  AUTHORS   Zhang,S.D., Kassis,J., Olde,B., Mellerick,D.M. and Odenwald,W.F.
  TITLE     Pollux, a novel Drosophila adhesion molecule, belongs to a family
            of proteins expressed in plants, yeast, nematodes, and man
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3214)
  AUTHORS   Zhang,S.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-MAR-1996) Shang-Ding Zhang, Neurogenetics, LNC,
            NINDS, NIH, 9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .3214
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                     /strain="Oregon R"
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     gene            1. .3214
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                     /protein_id="AAB02200.1"
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                     NMRTKYLPDMKKFQLQLYQLSRLVKDHLPDLYVWLDQNDVSPTLYAAPWILTVFSSQF
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                     LPEHVDKFVANIKSPLEVDSGVGTPLSPPSTASNSSGGSIFSRMGYRTTPPALSPLAQ
                     RQSYGVAITTAPCPQHMEEVAPATTMAVMPQEDVEEPQPMHPLSMVGGDVNVRFKGTT
                     QLKSIRPVHHMRAIPLGGVQHPSSTEPAVRVAPVPVELAPPAATATTGRS"
BASE COUNT      862 a    798 c    774 g    780 t
ORIGIN
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Query Match 8.6%; Score 304.6; DB 3; Length 3214;
Best Local Similarity 56.0%; Pred. No. 6.1e-56;
Matches 621; Conservative 0; Mismatches 479; Indels 9; Gaps 2;

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Qy   2155 gagctccgagagctgtggcaaaaggctattcttcaacagatactgctgcttagaatggag 2214
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Db    169 GAGCTGAGGGAACTGTGGCGCACTGCCATTAGGCAGACTATAATGCTGAACCGCATGGAG 228

Qy   2215 aaggaaaatcagaagctccaagcctctgaaaatgatttgctgaacaagcgcctgaagctc 2274
          | ||| ||    | | | ||  | |||||      |   |||||| | || ||
Db    229 ACGGAGAACGCCATGTTGCAGGCACGGCAGAATGAGAACGAGCTAAAGCGCATTAAACTG 288

Qy   2275 gattatgaagaaattactccctgtcttaaagaagtaactacagtgtgggaaaagatgctt 2334
          || || || || |||   |||||    ||  |  |||        |||||  ||||  ||
Db    289 GACTACGAGGAGATTGTACCCTGCGACAAGCAGCTAATCGAGCGATGGGAGCAGATCATT 348

Qy   2335 ---agcactccaggaagatcaaaaattaagtttgacatggaaaaaatgcactcggctgtt 2391
             |||   |   |    ||  |  |||   ||     ||    ||  |   ||  ||
Db    349 GAGCGCAACTCCACACAGATAGGCAACAAGAAGGATCCCAAAGTCCTGGGCCACGCCATT 408

Qy   2392 gggcaaggtgtgccacgtcatcaccgaggtgaaatctggaaatttctagctgagcaattc 2451
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Db    409 CGCACCGGAGTACCGCGATCGAAGCGCGGCGATGTCTGGACCTTCCTGGCTGAGCAGCAT 468

Qy   2452 caccttaa------acaccagtttcccagcaaacagcagccaaaggatgtgccatacaaa 2505
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Db    469 TCCATGAACACGGCACCGGTGGACACAAAGCGATTCCCCAACTTCAATACACCGTATCAC 528

Qy   2506 gaactcttaaagcagctgacttcccagcagcatgcgattcttattgaccttgggcgaacc 2565
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Db    529 ATGCTGCTGAAACACCTTACTGAGCATCAGCATGCGATTTTCATTGATCTGGGCAGGACT 588

Qy   2566 tttcctacacacccatacttctctgcccagcttggagcaggacagctatcgctttacaac 2625
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Db    589 TTTCCTAATCACCAGTTCTACAAGGATCCGCTTGGTCTCGGCCAGTTGTCGCTGTTTAAC 648

Qy   2626 attttgaaggcctactcacttctagaccaggaagtgggatattgccaaggtctcagcttt 2685
            |  ||||||| |||||  |||||||  | |||| | || || |||||  |||||  ||||
Db    649 CTGCTGAAGGCGTACTCCATTCTAGATCCGGAATTAGGGTACTGCCAGGGTCTGGGCTTC 708

Qy   2686 gtagcaggcattttgcttcttcatatgagtgaggaagaggcgtttaaaatgctcaagttt 2745
            |   ||| | || || || |||     ||| |   |  | ||| || |||| |||
Db    709 ATCTGCGGCGTCTTACTCCTGCATTGCGATGAAGCCAATTCATTTCAACTGCTGAAGCAC 768

Qy   2746 ctgatgtttgacatggggctgcggaaacagtatcggccagacatgattattttacagatc 2805
          || ||||||  |       |||| |    | || | ||| |||||||  |  || ||  |
Db    769 CTAATGTTTCGCCGTAATATGCGCACGAAATACCTGCCGGACATGAAAAAGTTTCAACTG 828

Qy   2806 cagatgtaccagctctcgaggttgcttcatgattaccacagagacctctacaatcacctg 2865
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Db    829 CAGCTGTATCAGCTCTCCCGATTGGTCAAGGATCATCTGCCAGATCTCTACGTGTGGCTC 888

Qy   2866 gaggagcacgagatcggccccagcctctacgctgccccctggttcctcaccatgtttgcc 2925
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Db    889 GATCAGAACGATGTCTCGCCCACTTTGTATGCGGCTCCATGGATCCTCACCGTCTTTAGC 948

Qy   2926 tcacagttcccgctgggattcgtagccagagtctttgatatgatttttcttcagggaaca 2985
          |||||||| |||||||||||||| ||| | ||||||||| || | || ||  |     |
Db    949 TCACAGTTTCCGCTGGGATTCGTGGCCCGCGTCTTTGATCTGCTCTTCCTGGAATCCTCC 1008

Qy   2986 gaggtcatatttaaagtggctttaagtctgttgggaagccataagcccttgattctgcag 3045
          || || || |||||  | ||  |      || |        || ||||      | |||
Db    1009 GATGTAATCTTTAAGTTTGCCATTGCCTTGCTCTCCGTGCACAAGCAGCAACTACTGGCC 1068

Qy   3046 catgaaaacctagaaaccatagttgactttataaaaagcacgctacccaaccttggcttg 3105
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Db    1069 AAGGATAACTTCGAAGAGATTATGGACTATCTGAAGACCGTGGTGCCAAAGATGGAGCAC 1128

Qy   3106 gtacagatggaaaagaccatcaatcaggtatttgaaatggacatcgctaaacagttacaa 3165
                |||||  | |  || || | ||| |||   |||||||| |  || ||| |
Db    1129 ACGTGCATGGAGCAAATTATGAAGCTGGTCTTTAGCATGGACATTGGAAAGCAGCTTGCC 1188

Qy   3166 gcttatgaagttgagtaccacgtccttcaagaagaacttatcgattcctctcctctcagt 3225
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Db    1189 GAATACAATGTGGAGTACAATGTGCTTCAGGAGGAGATTACCACCACTAACCATCACCTA 1248

Qy   3226 gacaaccaaagaatggataaattagagaa 3254
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Db    1249 GAAATGCTTAACCGGGAGAAGACGCAGAA 1277
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RESULT  15
DME17919
LOCUS       DME17919                4746 bp    mRNA    linear   INV 18-NOV-1998
DEFINITION  Drosophila melanogaster mRNA for pollux protein.
ACCESSION   Y17919
VERSION     Y17919.1  GI:3893102
KEYWORDS    pollux gene.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 4746)
  AUTHORS   Xu,X.Z., Wes,P.D., Chen,H., Li,H.S., Yu,M., Morgan,S., Liu,Y. and
            Montell,C.
  TITLE     Retinal targets for calmodulin include proteins implicated in
            synaptic transmission
  JOURNAL   J. Biol. Chem. 273 (47), 31297-31307 (1998)
  MEDLINE   99030403
REFERENCE   2  (bases 1 to 4746)
  AUTHORS   Montell,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-AUG-1998) C. Montell, The Johns Hopkins University
            School of Medicine, Department of Biological Chermistry, 725 N.
            Wolfe Street, Baltimore, MD 21205-2185, USA
FEATURES             Location/Qualifiers
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                     /map="83C"
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     CDS             452. .4591
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BASE COUNT 1211 a 1342 c 1261 g 932 t
ORIGIN

Query Match 8.6%; Score 304.6; DB 3; Length 4746;
Best Local Similarity 56.0%; Pred. No. 6.4e-56;
Matches 621; Conservative 0; Mismatches 479; Indels 9; Gaps 2;

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Db   2432 GAGCTGAGGGAACTGTGGCGCACTGCCATTAGGCAGACTATAATGCTGAACCGCATGGAG 2491

Qy   2215 aaggaaaatcagaagctccaagcctctgaaaatgatttgctgaacaagcgcctgaagctc 2274
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Db   2492 ACGGAGAACGCCATGTTGCAGGCACGGCAGAATGAGAACGAGCTAAAGCGCATTAAACTG 2551

Qy   2275 gattatgaagaaattactccctgtcttaaagaagtaactacagtgtgggaaaagatgctt 2334
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Db   2552 GACTACGAGGAGATTGTACCCTGCGACAAGCAGCTAATCGAGCGATGGGAGCAGATCATT 2611

Qy   2335 ---agcactccaggaagatcaaaaattaagtttgacatggaaaaaatgcactcggctgtt 2391
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Db   2612 GAGCGCAACTCCACACAGATAGGCAACAAGAAGGATCCCAAAGTCCTGGGCCACGCCATT 2671

Qy   2392 gggcaaggtgtgccacgtcatcaccgaggtgaaatctggaaatttctagctgagcaattc 2451
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Db   2672 CGCACCGGAGTACCGCGATCGAAGCGCGGCGATGTCTGGACCTTCCTGGCTGAGCAGCAT 2731

Qy   2452 caccttaa------acaccagtttcccagcaaacagcagccaaaggatgtgccatacaaa 2505
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Qy   2506 gaactcttaaagcagctgacttcccagcagcatgcgattcttattgaccttgggcgaacc 2565
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Db   2792 ATGCTGCTGAAACACCTTACTGAGCATCAGCATGCGATTTTCATTGATCTGGGCAGGACT 2851

Qy   2566 tttcctacacacccatacttctctgcccagcttggagcaggacagctatcgctttacaac 2625
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Qy   2686 gtagcaggcattttgcttcttcatatgagtgaggaagaggcgtttaaaatgctcaagttt 2745
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Db   2972 ATCTGCGGCGTCTTACTCCTGCATTGCGATGAAGCCAATTCATTTCAACTGCTGAAGCAC 3031

Qy   2746 ctgatgtttgacatggggctgcggaaacagtatcggccagacatgattattttacagatc 2805
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Db   3032 CTAATGTTTCGCCGTAATATGCGCACGAAATACCTGCCGGACATGAAAAAGTTTCAACTG 3091

Qy   2806 cagatgtaccagctctcgaggttgcttcatgattaccacagagacctctacaatcacctg 2865
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Db   3092 CAGCTGTATCAGCTCTCCCGATTGGTCAAGGATCATCTGCCAGATCTCTACGTGTGGCTC 3151

Qy   2866 gaggagcacgagatcggccccagcctctacgctgccccctggttcctcaccatgtttgcc 2925
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Db   3152 GATCAGAACGATGTCTCGCCCACTTTGTATGCGGCTCCATGGATCCTCACCGTCTTTAGC 3211

Qy   2926 tcacagttcccgctgggattcgtagccagagtctttgatatgatttttcttcagggaaca 2985
          |||||||| |||||||||||||| ||| | |||||||| || | || ||  |     |
Db   3212 TCACAGTTTCCGCTGGGATTCGTGGCCCGCGTCTTTGATCTGCTCTTCCTGGAATCCTCC 3271

Qy   2986 gaggtcatatttaaagtggctttaagtctgttgggaagccataagcccttgattctgcag 3045
          || || || |||||  | ||  |     || |       || ||||       | |||
Db   3272 GATGTAATCTTTAAGTTTGCCATTGCCTTGCTCTCCGTGCACAAGCAGCAACTACTGGCC 3331

Qy   3046 catgaaaacctagaaaccatagttgacttttataaaaagcacgctacccaaccttggcttg 3105
           | || ||| | |||    ||  | |||| | | || | |  | | || ||  | |
Db   3332 AAGGATAACTTCGAAGAGATTATGGACTATCTGAAGACCGTGGTGCCAAAGATGGAGCAC 3391

Qy   3106 gtacagatggaaaagaccatcaatcaggtatttgaaatggacatcgctaaacagttacaa 3165
               |||||  | |  || || | ||| |||   |||||||| |  || ||| |
Db   3392 ACGTGCATGGAGCAAATTATGAAGCTGGTCTTTAGCATGGACATTGGAAAGCAGCTTGCC 3451

Qy   3166 gcttatgaagttgagtaccacgtccttcaagaagaacttatcgattcctctcctctcagt 3225
          |  ||  | || |||||| | || ||||| || ||  ||| |    |    | || |
Db   3452 GAATACAATGTGGAGTACAATGTGCTTCAGGAGGAGATTACCACCACTAACCATCACCTA 3511

Qy   3226 gacaaccaaagaatggataaattagagaa 3254
          || |  |  |    ||| ||     ||||
Db   3512 GAAATGCTTAACCGGGAGAAGACGCAGAA 3540
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Job time: 17490 sec